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(54) Title: CHLAMYDIA PNEUMONIAE GENOME SEQUENCE			
(57) Abstract  <p><i>C. pneumoniae</i> genome sequence and analysis of the encoded polypeptides and RNAs are provided. The <i>C. pneumoniae</i> gene nucleic acid compositions find use in identifying homologous or related proteins and the DNA sequences encoding such proteins; in producing compositions that modulate the expression or function of the protein; and in studying associated physiological pathways. In addition, modulation of the gene activity <i>in vivo</i> is used for prophylactic and therapeutic purposes, such as identification of cell type based on expression, and the like.</p>			
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WO 00/27994

PCT/US99/26923

## CHLAMYDIA PNEUMONIAE GENOME SEQUENCE

### CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to 60/128,606, filed April 8, 1999 and  
5 60/108,279, filed November 12, 1998, which are incorporated herein by reference.

### STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

### 10 FIELD OF THE INVENTION

This invention relates to nucleic acids and polypeptides from *Chlamydia pneumoniae* and to their use in the diagnosis, prevention and treatment of diseases associated with *C. pneumoniae*.

### 15 BACKGROUND OF THE INVENTION

*Chlamydiaceae* is a family of obligate intracellular parasite with a tropism for epithelial cells lining the mucus membranes. The bacteria have two morphologically distinct forms, "elementary body" and "reticulate body". The elementary body is the infectious form, and has a rigid cell wall, primarily of cross-linked outer membrane  
20 proteins. The reticulate body is the intracellular, metabolically active form. A unique developmental cycle between these two forms characterizes *Chlamydia* growth.

*C. pneumoniae* is a human respiratory pathogen that causes acute respiratory disease, and approximately 10% of community-acquired pneumonia. Antibody prevalence studies have shown that virtually everyone is infected with *C.  
25 pneumoniae* at some time, and that reinfection is common. In addition to respiratory disease, studies have shown an association of this organism with coronary artery disease. It has been demonstrated in atherosclerotic lesions of the aorta and coronary arteries by immunocytochemistry and by polymerase chain reaction (Kuo *et al.* (1993) J Infect Dis 167(4):841-849).

30 Recent reports have further demonstrated the presence of *C. pneumoniae* in the walls of abdominal aortic aneurysms (Juvonen *et al.* (1997) J Vasc Surg 25(3):499-505). Abdominal aortic aneurysms are frequently associated with atherosclerosis, and inflammation may be an important factor in aneurysmal dilatation.

WO 00/27994

PCT/US99/26923

*C. pneumoniae* may play a role in maintaining an inflammation and triggering the development of aortic aneurysms.

Muhlestein *et al.* (1996) JACC 27:1555-61, reported a differential incidence of *Chlamydia* species within the coronary artery wall of patients with atherosclerosis versus those with other forms of cardiovascular disease. The extremely high rate of possible infection in patients with symptomatic atherosclerotic disease compared to the very low rate in patients with normal coronary arteries or coronary artery disease from chronic transplant rejection provides evidence for a direct link between the atherosclerotic process and *Chlamydia* infection. Because a history of chlamydial infection is so prevalent in the population, the issue of causality remains. On a physiologic and pathologic level, abnormal interactions among endothelial cells, platelets, macrophages and lymphocytes may lead to a cascade of events resulting in acute endothelial damage, thrombosis and repair, chronically leading to the development of atheroma in blood vessels.

*C. pneumoniae* is related to other *Chlamydia* species, but the level of sequence similarity is relatively low. Very little is known about the biology of this organism, although it appears to be an important human pathogen. Allelic diversity and structural relationships between specific genes of Chlamydial species is described in Kaltenboeck *et al.* (1993) J Bacteriol 175(2):487-502; Gaydos *et al.* (1992) Infect Immun 60(12):5319-5323; Everett *et al.* (1997) Int J Syst Bacteriol 47(2):461-473; and Pudjiatmoko *et al.* (1997) Int J Syst Bacteriol 47(2):425-431.

A number of studies have been published describing methods for detection of *C. pneumoniae*, and for distinguishing between Chlamydial species. Such methods include PCR detection (Rasmussen *et al.* (1992) Mol Cell Probes 6(5):389-394; Holland *et al.* (1990) J Infect Dis 162(4):984-987); a simplified polymerase chain reaction-enzyme immunoassay (Wilson *et al.* (1996) J Appl Bacteriol 80(4):431-438); sequence determination and restriction endonuclease cleavage (Herrmann *et al.* (1996) J Clin Microbiol 34(8):1897-1902).

Antigenic and molecular analyses of different *C. pneumoniae* strains is described in Jantos *et al.* (1997) J Clin Microbiol 35(3):620-623. Some genes of *C. pneumoniae* have been isolated and sequenced. These include the Gro E operon (Kikuta *et al.* (1991) Infect Immun 59(12):4665-4669); the major outer membrane protein Perez *et*



WO 00/27994

PCT/US99/26923

*al.* (1991) Infect Immun 59(6):2195-2199; the DnaK protein homolog (Kornak *et al.* (1991) Infect Immun 59(2):721-725); as well as a number of ribosomal and other genes.

5

## SUMMARY OF THE INVENTION

This invention provides the genomic sequence of *Chlamydia pneumoniae*.

The sequence information is useful for a variety of diagnostic and analytical methods.

The genomic sequence may be embodied in a variety of media, including computer

10 readable forms, or as a nucleic acid comprising a selected fragment of the sequence.

Such fragments generally consist of an open reading frame, transcriptional or translational control elements, or fragments derived therefrom. Proteins encoded by the open reading frames are useful for diagnostic purposes, as well as for their enzymatic or structural activity.

15

## DEFINITIONS

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those

20 encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline,  $\gamma$ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an  $\alpha$  carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group., e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl

25 sulfonium Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

30

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

WO 00/27994

PCT/US99/26923

"Amplification" primers are oligonucleotides comprising either natural or analogue nucleotides that can serve as the basis for the amplification of a select nucleic acid sequence. They include, e.g., polymerase chain reaction primers and ligase chain reaction oligonucleotides.

5 "Antibody" refers to an immunoglobulin molecule able to bind to a specific epitope on an antigen. Antibodies can be a polyclonal mixture or monoclonal. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. Antibodies may exist in a variety of forms including, for example, Fv, F<sub>ab</sub>, and F(ab)<sub>2</sub>, as  
10 well as in single chains. Single-chain antibodies, in which genes for a heavy chain and a light chain are combined into a single coding sequence, may also be used.

An "antigen" is a molecule that is recognized and bound by an antibody, e.g., peptides, carbohydrates, organic molecules, or more complex molecules such as glycolipids and glycoproteins. The part of the antigen that is the target of antibody  
15 binding is an antigenic determinant and a small functional group that corresponds to a single antigenic determinant is called a hapten.

"Biological sample" refers to any sample obtained from a living or dead organism. Examples of biological samples include biological fluids and tissue specimens. Such biological samples can be prepared for analysis of the presence of *C. pneumoniae*  
20 nucleic acids, proteins, or antibodies specifically reactive with the proteins.

The term "*C. pneumoniae* gene" shall be intended to mean the open reading frame encoding specific *C. pneumoniae* polypeptides, as well as adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 2 kb beyond the coding region, but possibly further in either direction. The gene may be  
25 introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially  
30 identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues

WO 00/27994

PCT/US99/26923

(Batzner *et al.*, *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8:91-98 (1994)). Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all  
5 encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the  
10 nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

15 As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid.  
20 Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following groups each contain amino acids that are conservative substitutions for one another:

- 25 1) Alanine (A), Glycine (G);  
2) Serine (S), Threonine (T);  
3) Aspartic acid (D), Glutamic acid (E);  
4) Asparagine (N), Glutamine (Q);  
5) Cysteine (C), Methionine (M);  
30 6) Arginine (R), Lysine (K), Histidine (H);  
7) Isoleucine (I), Leucine (L), Valine (V); and  
8) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).  
*see, e.g., Creighton, Proteins (1984)).*

WO 00/27994

PCT/US99/26923

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition also refers to the complement of a test sequence, which has a designated percent sequence or subsequence complementarity when the test sequence has a designated or substantial identity to a reference sequence. For example, a designated amino acid percent identity of 95% refers to sequences or subsequences that have at least about 95% amino acid identity when aligned for maximum correspondence over a comparison window as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Such sequences would then be said to have substantial identity, or to be substantially identical to each other. Preferably, sequences have at least about 70% identity, more preferably 80% identity, more preferably 90-95% identity and above. Preferably, the percent identity exists over a region of the sequence that is at least about 25 amino acids in length, more preferably over a region that is 50-100 amino acids in length.

When percentage of sequence identity is used in reference to proteins or peptides, it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions, where amino acids residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated according to, e.g., the algorithm of Meyers & Miller, *Computer Applic. Biol. Sci.* 4:11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA)..

WO 00/27994

PCT/US99/26923

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated or default program parameters.

A comparison window includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 25 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Ausubel et al., supra*).

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a tree or dendrogram showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J. Mol. Evol.* 35:351-360 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The

WO 00/27994

PCT/US99/26923

final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, e.g, version 7.0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984)).

Another example of algorithm that is suitable for determining percent sequence identity (i.e., substantial similarity or identity) is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al. supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues, always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as default parameters a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

WO 00/27994

PCT/US99/26923

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.,* Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ( $P(N)$ ), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

10 An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below.

Another indication that polynucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically stringent conditions for a Southern blot protocol involve hybridizing in a buffer comprising 5x SSC, 1% SDS at 65°C or hybridizing in a buffer containing 5x SSC and 1% SDS at 42°C and washing at 65°C with a 0.2x SSC, 0.1% SDS wash.

A "label" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include  $^{32}P$ , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, dioxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available.

WO 00/27994

PCT/US99/26923

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which  
5 have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

Unless otherwise indicated, a particular nucleic acid sequence also  
10 implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a  
15 nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester  
20 bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably  
25 directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

A labeled nucleic acid probe or oligonucleotide is one that is bound, either  
30 covalently, through a linker, or through ionic, van der Waals or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.



WO 00/27994

PCT/US99/26923

"Pharmaceutically acceptable" means a material that is not biologically or otherwise undesirable, i.e., the material can be administered to an individual along with a *Chlamydia* antigen without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition.

5           The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an analog or mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

10           The phrase "specifically or selectively hybridizing to," refers to hybridization between a probe and a target sequence in which the probe binds substantially only to the target sequence, forming a hybridization complex, when the target is in a heterogeneous mixture of polynucleotides and other compounds. Such hybridization is determinative of the presence of the target sequence. Although the probe  
15           may bind other unrelated sequences, at least 90%, preferably 95% or more of the hybridization complexes formed are with the target sequence.

          The term "recombinant" when used with reference to a cell, or nucleic acid, or vector, indicates that the cell, or nucleic acid, or vector, has been modified by the introduction of a heterologous nucleic acid or the alteration of a native nucleic acid, or  
20           that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

          The phrase "specifically immunoreactive with", when referring to a protein  
25           or peptide, refers to a binding reaction between the protein and an antibody which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other compounds. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such  
30           conditions may require an antibody that is selected for its specificity for a particular protein. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein and are described in detail below.

WO 00/27994

PCT/US99/26923

The phrase "substantially pure" or "isolated" when referring to a *Chlamydia* peptide or protein, means a chemical composition which is free of other subcellular components of the *Chlamydia* organism. Typically, a monomeric protein is substantially pure when at least about 85% or more of a sample exhibits a single polypeptide backbone. Minor variants or chemical modifications may typically share the same polypeptide sequence. Depending on the purification procedure, purities of 85%, and preferably over 95% pure are possible. Protein purity or homogeneity may be indicated by a number of means well known in the art, such as polyacrylamide gel electrophoresis of a protein sample, followed by visualizing a single polypeptide band on a polyacrylamide gel upon silver staining. For certain purposes high resolution will be needed and HPLC or a similar means for purification utilized.

#### DETAILED DESCRIPTION

The present invention provides the nucleotide sequence of the *C. pneumoniae* genome SEQ ID NO: 1 or a representative fragment thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. As used herein, a "representative fragment" of the nucleotide sequence depicted in SEQ ID NO: 1 refers to any portion which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are open reading frames, expression modulating fragments, uptake modulating fragments, and fragments which can be used to diagnose the presence of *C. pneumoniae* in sample. Using the information provided in the present application, together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *C. pneumoniae* proteins. A non-limiting identification of such preferred representative fragments is provided in Tables 2 and 3.

#### Diagnostic use of *C. pneumoniae* nucleic acids

##### Hybridization-based assays

Using the nucleic acids disclosed here, one of skill can design nucleic acid hybridization-based assays for the detection of *C. pneumoniae*. Any of a number of well known techniques for the specific detection of target nucleic acids can be used. Exemplary hybridization-based assays include, but are not limited to, traditional "direct

WO 00/27994

PCT/US99/26923

probe" methods such as Southern Blots, dot blots, *in situ* hybridization (e.g., FISH), PCR, and the like. The methods can be used in a wide variety of formats including, but not limited to substrate- (e.g. membrane or glass) bound methods or array-based approaches as described below. As noted above, this invention also embraces methods for detecting the presence of *Chlamydia* DNA or RNA in biological samples. These sequences can be used to detect *Chlamydia* in biological samples from patients suspected of being infected. A variety of methods of specific DNA and RNA measurement using nucleic acid hybridization techniques are known to those of skill in the art (see Sambrook *et al.*, *supra*).

10                    *In situ* hybridization assays are well known (e.g., Angerer (1987) *Meth. Enzymol* 152: 649). Generally, *in situ* hybridization comprises the following major steps: (1) fixation of tissue or biological structure to be analyzed; (2) prehybridization treatment of the biological structure to increase accessibility of target DNA, and to reduce nonspecific binding; (3) hybridization of the mixture of nucleic acids to the nucleic acid in the biological structure or tissue; (4) post-hybridization washes to remove nucleic acid fragments not bound in the hybridization and (5) detection of the hybridized nucleic acid fragments. The reagent used in each of these steps and the conditions for use vary depending on the particular application.

20                    In a typical *in situ* hybridization assay, cells are fixed to a solid support, typically a glass slide. If a nucleic acid is to be probed, the cells are typically denatured with heat or alkali. The cells are then contacted with a hybridization solution at a moderate temperature to permit annealing of labeled probes specific to the nucleic acid sequence encoding the protein. The targets (e.g., cells) are then typically washed at a predetermined stringency or at an increasing stringency until an appropriate signal to noise ratio is obtained.

25                    The nucleic acids of this invention are particularly well suited to array-based hybridization formats. Arrays are a multiplicity of different "probe" or "target" nucleic acids (or other compounds) attached to one or more surfaces (e.g., solid, membrane, or gel). In a preferred embodiment, the multiplicity of nucleic acids (or other moieties) is attached to a single contiguous surface or to a multiplicity of surfaces juxtaposed to each other.

30                    In an array format a large number of different hybridization reactions can be run essentially "in parallel." This provides rapid, essentially simultaneous, evaluation

WO 00/27994

PCT/US99/26923

of a number of hybridizations in a single "experiment". Methods of performing hybridization reactions in array based formats are well known to those of skill in the art (see, e.g., Pastinen (1997) *Genome Res.* 7: 606-614; Jackson (1996) *Nature Biotechnology* 14:1685; Chee (1995) *Science* 274: 610; WO 96/17958.

- 5                   Arrays, particularly nucleic acid arrays can be produced according to a wide variety of methods well known to those of skill in the art. For example, in a simple embodiment, "low density" arrays can simply be produced by spotting (e.g. by hand using a pipette) different nucleic acids at different locations on a solid support (e.g. a glass surface, a membrane, etc.).
- 10                   This simple spotting, approach has been automated to produce high density spotted arrays (see, e.g., U.S. Patent No. 5,807,522). This patent describes the use of an automated systems that taps a microcapillary against a surface to deposit a small volume of a biological sample. The process is repeated to generate high density arrays. Arrays can also be produced using oligonucleotide synthesis technology. Thus, for
- 15                   example, U.S. Patent No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092 teach the use of light-directed combinatorial synthesis of high density oligonucleotide arrays.

- Many methods for immobilizing nucleic acids on a variety of solid surfaces are known in the art. A wide variety of organic and inorganic polymers, as well
- 20                   as other materials, both natural and synthetic, can be employed as the material for the solid surface. Illustrative solid surfaces include, e.g., nitrocellulose, nylon, glass, quartz, diazotized membranes (paper or nylon), silicones, polyformaldehyde, cellulose, and cellulose acetate. In addition, plastics such as polyethylene, polypropylene, polystyrene, and the like can be used. Other materials which may be employed include paper,
- 25                   ceramics, metals, metalloids, semiconductive materials, cermets or the like. In addition, substances that form gels can be used. Such materials include, e.g., proteins (e.g., gelatins), lipopolysaccharides, silicates, agarose and polyacrylamides. Where the solid surface is porous, various pore sizes may be employed depending upon the nature of the system.

- 30                   In preparing the surface, a plurality of different materials may be employed, particularly as laminates, to obtain various properties. For example, proteins (e.g., bovine serum albumin) or mixtures of macromolecules (e.g., Denhardt's solution) can be employed to avoid non-specific binding, simplify covalent conjugation, enhance

WO 00/27994

PCT/US99/26923

signal detection or the like. If covalent bonding between a compound and the surface is desired, the surface will usually be polyfunctional or be capable of being polyfunctionalized. Functional groups which may be present on the surface and used for linking can include carboxylic acids, aldehydes, amino groups, cyano groups, ethylenic groups, hydroxyl groups, mercapto groups and the like. The manner of linking a wide variety of compounds to various surfaces is well known and is amply illustrated in the literature.

For example, methods for immobilizing nucleic acids by introduction of various functional groups to the molecules is known (*see, e.g., Bischoff (1987) Anal. Biochem.*, 164: 336-344; Kremsky (1987) *Nucl. Acids Res.* 15: 2891-2910). Modified nucleotides can be placed on the target using PCR primers containing the modified nucleotide, or by enzymatic end labeling with modified nucleotides. Use of glass or membrane supports (*e.g., nitrocellulose, nylon, polypropylene*) for the nucleic acid arrays of the invention is advantageous because of well developed technology employing manual and robotic methods of arraying targets at relatively high element densities. Such membranes are generally available and protocols and equipment for hybridization to membranes is well known.

Target elements of various sizes, ranging from 1 mm diameter down to 1  $\mu\text{m}$  can be used. Smaller target elements containing low amounts of concentrated, fixed probe DNA are used for high complexity comparative hybridizations since the total amount of sample available for binding to each target element will be limited. Thus it is advantageous to have small array target elements that contain a small amount of concentrated probe DNA so that the signal that is obtained is highly localized and bright. Such small array target elements are typically used in arrays with densities greater than  $10^4/\text{cm}^2$ . Relatively simple approaches capable of quantitative fluorescent imaging of  $1\text{ cm}^2$  areas have been described that permit acquisition of data from a large number of target elements in a single image (*see, e.g., Wittrup (1994) Cytometry* 16:206-213).

If fluorescently labeled nucleic acid samples are used, arrays on solid surface substrates with much lower fluorescence than membranes, such as glass, quartz, or small beads, can achieve much better sensitivity. Substrates such as glass or fused silica are advantageous in that they provide a very low fluorescence substrate, and a highly efficient hybridization environment. Covalent attachment of the target nucleic acids to glass or synthetic fused silica can be accomplished according to a number of

WO 00/27994

PCT/US99/26923

known techniques (described above). Nucleic acids can be conveniently coupled to glass using commercially available reagents. For instance, materials for preparation of silanized glass with a number of functional groups are commercially available or can be prepared using standard techniques (see, e.g., Gait (1984) *Oligonucleotide Synthesis: A Practical Approach*, IRL Press, Wash., D.C.). Quartz cover slips, which have at least 10-fold lower autofluorescence than glass, can also be silanized.

Alternatively, probes can also be immobilized on commercially available coated beads or other surfaces. For instance, biotin end-labeled nucleic acids can be bound to commercially available avidin-coated beads. Streptavidin or anti-digoxigenin antibody can also be attached to silanized glass slides by protein-mediated coupling using e.g., protein A following standard protocols (see, e.g., Smith (1992) *Science* 258: 1122-1126). Biotin or digoxigenin end-labeled nucleic acids can be prepared according to standard techniques. Hybridization to nucleic acids attached to beads is accomplished by suspending them in the hybridization mix, and then depositing them on the glass substrate for analysis after washing. Alternatively, paramagnetic particles, such as ferric oxide particles, with or without avidin coating, can be used.

A variety of other nucleic acid hybridization formats are known to those skilled in the art. For example, common formats include sandwich assays and competition or displacement assays. Hybridization techniques are generally described in Hames and Higgins (1985) *Nucleic Acid Hybridization, A Practical Approach*, IRL Press; Gall and Pardue (1969) *Proc. Natl. Acad. Sci. USA* 63: 378-383; and John *et al.* (1969) *Nature* 223: 582-587.

Sandwich assays are commercially useful hybridization assays for detecting or isolating nucleic acid sequences. Such assays utilize a "capture" nucleic acid covalently immobilized to a solid support and a labeled "signal" nucleic acid in solution. The sample will provide the target nucleic acid. The "capture" nucleic acid and "signal" nucleic acid probe hybridize with the target nucleic acid to form a "sandwich" hybridization complex. To be most effective, the signal nucleic acid should not hybridize with the capture nucleic acid.

Detection of a hybridization complex may require the binding of a signal generating complex to a duplex of target and probe polynucleotides or nucleic acids. Typically, such binding occurs through ligand and anti-ligand interactions as between a ligand-conjugated probe and an anti-ligand conjugated with a signal.

WO 00/27994

PCT/US99/26923

The sensitivity of the hybridization assays may be enhanced through use of a nucleic acid amplification system that multiplies the target nucleic acid being detected. Examples of such systems include the polymerase chain reaction (PCR) system and the ligase chain reaction (LCR) system. Other methods recently described in the art are the  
5 nucleic acid sequence based amplification (NASBAO, Cangene, Mississauga, Ontario) and Q Beta Replicase systems.

Nucleic acid hybridization simply involves providing a denatured probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. The nucleic acids  
10 that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids, or in the addition of chemical agents, or the raising of the pH. Under low stringency conditions  
15 (*e.g.*, low temperature and/or high salt and/or high target concentration) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches.

One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency to ensure hybridization and then subsequent washes are performed at higher stringency to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25  
25 X SSPE-T at 37°C to 70°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present.

In general, there is a tradeoff between hybridization specificity  
30 (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher

WO 00/27994

PCT/US99/26923

stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular probes of interest.

Methods of optimizing hybridization conditions are well known to those of skill in the art (*see, e.g.,* Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24: Hybridization With Nucleic Acid Probes*, Elsevier, N.Y.).

Labeling and detection of nucleic acids.

In a preferred embodiment, the hybridized nucleic acids are detected by detecting one or more labels attached to the sample or probe nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. Means of attaching labels to nucleic acids include, for example nick translation or end-labeling (*e.g.* with a labeled RNA) by kinasing of the nucleic acid and subsequent attachment (ligation) of a nucleic acid linker joining the sample nucleic acid to a label (*e.g.*, a fluorophore). A wide variety of linkers for the attachment of labels to nucleic acids are also known. In addition, intercalating dyes and fluorescent nucleotides can also be used.

Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (*e.g.*, Dynabeads<sup>TM</sup>), fluorescent dyes (*e.g.*, fluorescein, texas red, rhodamine, green fluorescent protein, and the like, *see, e.g.*, Molecular Probes, Eugene, Oregon, USA), radiolabels (*e.g.*, <sup>3</sup>H, <sup>125</sup>I, <sup>35</sup>S, <sup>14</sup>C, or <sup>32</sup>P), enzymes (*e.g.*, horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold (*e.g.*, gold particles in the 40 -80 nm diameter size range scatter green light with high efficiency) or colored glass or plastic (*e.g.*, polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241.

A fluorescent label is preferred because it provides a very strong signal with low background. It is also optically detectable at high resolution and sensitivity through a quick scanning procedure. The nucleic acid samples can all be labeled with a single label, *e.g.*, a single fluorescent label. Alternatively, in another embodiment, different nucleic acid samples can be simultaneously hybridized where each nucleic acid



WO 00/27994

PCT/US99/26923

sample has a different label. For instance, one target could have a green fluorescent label and a second target could have a red fluorescent label. The scanning step will distinguish sites of binding of the red label from those binding the green fluorescent label. Each nucleic acid sample (target nucleic acid) can be analyzed independently from one another.

5            Suitable chromogens which can be employed include those molecules and compounds which absorb light in a distinctive range of wavelengths so that a color can be observed or, alternatively, which emit light when irradiated with radiation of a particular wave length or wave length range, *e.g.*, fluorescers.

Desirably, fluorescers should absorb light above about 300 nm, preferably  
10    about 350 nm, and more preferably above about 400 nm, usually emitting at wavelengths greater than about 10 nm higher than the wavelength of the light absorbed. It should be noted that the absorption and emission characteristics of the bound dye can differ from the unbound dye. Therefore, when referring to the various wavelength ranges and characteristics of the dyes, it is intended to indicate the dyes as employed and not the dye  
15    which is unconjugated and characterized in an arbitrary solvent.

Fluorescers are generally preferred because by irradiating a fluorescer with light, one can obtain a plurality of emissions. Thus, a single label can provide for a plurality of measurable events.

Detectable signal can also be provided by chemiluminescent and  
20    bioluminescent sources. Chemiluminescent sources include a compound which becomes electronically excited by a chemical reaction and can then emit light which serves as the detectable signal or donates energy to a fluorescent acceptor. Alternatively, luciferins can be used in conjunction with luciferase or lucigenins to provide bioluminescence. Spin labels are provided by reporter molecules with an unpaired electron spin which can  
25    be detected by electron spin resonance (ESR) spectroscopy. Exemplary spin labels include organic free radicals, transitional metal complexes, particularly vanadium, copper, iron, and manganese, and the like. Exemplary spin labels include nitroxide free radicals.

The label may be added to the target (sample) nucleic acid(s) prior to, or  
30    after the hybridization. So called "direct labels" are detectable labels that are directly attached to or incorporated into the target (sample) nucleic acid prior to hybridization. In contrast, so called "indirect labels" are joined to the hybrid duplex after hybridization. Often, the indirect label is attached to a binding moiety that has been attached to the

WO 00/27994

PCT/US99/26923

target nucleic acid prior to the hybridization. Thus, for example, the target nucleic acid may be biotinylated before the hybridization. After hybridization, an avidin-conjugated fluorophore will bind the biotin bearing hybrid duplexes providing a label that is easily detected. For a detailed review of methods of labeling nucleic acids and detecting labeled  
5 hybridized nucleic acids see *Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24: Hybridization With Nucleic Acid Probes*, P. Tijssen, ed. Elsevier, N.Y., (1993)).

Fluorescent labels are easily added during an *in vitro* transcription reaction. Thus, for example, fluorescein labeled UTP and CTP can be incorporated into  
10 the RNA produced in an *in vitro* transcription.

The labels can be attached directly or through a linker moiety. In general, the site of label or linker-label attachment is not limited to any specific position. For example, a label may be attached to a nucleoside, nucleotide, or analogue thereof at any position that does not interfere with detection or hybridization as desired. For example,  
15 certain Label-ON Reagents from Clontech (Palo Alto, CA) provide for labeling interspersed throughout the phosphate backbone of an oligonucleotide and for terminal labeling at the 3' and 5' ends. As shown for example herein, labels can be attached at positions on the ribose ring or the ribose can be modified and even eliminated as desired. The base moieties of useful labeling reagents can include those that are naturally  
20 occurring or modified in a manner that does not interfere with the purpose to which they are put. Modified bases include but are not limited to 7-deaza A and G, 7-deaza-8-aza A and G, and other heterocyclic moieties.

It will be recognized that fluorescent labels are not to be limited to single species organic molecules, but include inorganic molecules, multi-molecular mixtures of  
25 organic and/or inorganic molecules, crystals, heteropolymers, and the like. Thus, for example, CdSe-CdS core-shell nanocrystals enclosed in a silica shell can be easily derivatized for coupling to a biological molecule (Bruchez *et al.* (1998) *Science*, 281: 2013-2016). Similarly, highly fluorescent quantum dots (zinc sulfide-capped cadmium selenide) have been covalently coupled to biomolecules for use in ultrasensitive  
30 biological detection (Warren and Nie (1998) *Science*, 281: 2016-2018).

#### Amplification-based assays.

In another embodiment, amplification-based assays can be used to detect nucleic acids. In such amplification-based assays, the nucleic acid sequences act as a

WO 00/27994

PCT/US99/26923

template in an amplification reaction (e.g. Polymerase Chain Reaction (PCR)). Detailed protocols for quantitative PCR are provided in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Other suitable amplification methods include, but are not limited to ligase  
5 chain reaction (LCR) (see Wu and Wallace (1989) *Genomics* 4: 560, Landegren *et al.* (1988) *Science* 241: 1077, and Barringer *et al.* (1990) *Gene* 89: 117, transcription amplification (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86: 1173), and self-sustained sequence replication (Guatelli *et al.* (1990) *Proc. Nat. Acad. Sci. USA* 87: 1874).

10                   Detection of *C. pneumoniae* gene expression

The nucleic acids of the invention can also be used to *C. pneumoniae* detect gene transcripts. Methods of detecting and/or quantifying gene transcripts using nucleic acid hybridization techniques are known to those of skill in the art (see Sambrook *et al. supra*). For example, a Northern transfer may be used for the detection of the  
15 desired mRNA directly. In brief, the mRNA is isolated from a given cell sample using, for example, an acid guanidinium-phenol-chloroform extraction method. The mRNA is then electrophoresed to separate the mRNA species and the mRNA is transferred from the gel to a nitrocellulose membrane. As with the Southern blots, labeled probes are used to identify and/or quantify the target mRNA.

20                   In another preferred embodiment, the gene transcript can be measured using amplification (e.g. PCR) based methods as described above for directly assessing copy number of the target sequences.

Expression of *C. pneumoniae* proteins

The nucleic acids disclosed here can be used for recombinant expression  
25 of the proteins. In these methods, the nucleic acids encoding the proteins of interest are introduced into suitable host cells, followed by induction of the cells to produce large amounts of the protein. The invention relies on routine techniques in the field of recombinant genetics, well known to those of ordinary skill in the art. A basic text disclosing the general methods of use in this invention is Sambrook *et al.*, *Molecular*  
30 *Cloning, A Laboratory Manual* (2nd ed. 1989).

Standard transfection methods are used to produce prokaryotic, mammalian, yeast or insect cell lines which express large quantities of the desired

WO 00/27994

PCT/US99/26923

polypeptide, which is then purified using standard techniques (*see, e.g., Colley et al., J. Biol. Chem.* 264:17619-17622, 1989; *Guide to Protein Purification, supra*).

5 The nucleotide sequences used to transfect the host cells can be modified to yield *Chlamydia* polypeptides with a variety of desired properties. For example, the polypeptides can vary from the naturally-occurring sequence at the primary structure level by amino acid, insertions, substitutions, deletions, and the like. These modifications can be used in a number of combinations to produce the final modified protein chain.

The amino acid sequence variants can be prepared with various objectives in mind, including facilitating purification and preparation of the recombinant  
10 polypeptide. The modified polypeptides are also useful for modifying plasma half life, improving therapeutic efficacy, and lessening the severity or occurrence of side effects during therapeutic use. The amino acid sequence variants are usually predetermined variants not found in nature but exhibit the same immunogenic activity as naturally occurring protein. In general, modifications of the sequences encoding the polypeptides  
15 may be readily accomplished by a variety of well-known techniques, such as site-directed mutagenesis (*see Gillman & Smith, Gene* 8:81-97 (1979); *Roberts et al., Nature* 328:731-734 (1987)). One of ordinary skill will appreciate that the effect of many mutations is difficult to predict. Thus, most modifications are evaluated by routine screening in a suitable assay for the desired characteristic. For instance, the effect of various  
20 modifications on the ability of the polypeptide to elicit a protective immune response can be easily determined using *in vitro* assays. For instance, the polypeptides can be tested for their ability to induce lymphoproliferation, T cell cytotoxicity, or cytokine production using standard techniques.

The particular procedure used to introduce the genetic material into the  
25 host cell for expression of the polypeptide is not particularly critical. Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA  
30 or other foreign genetic material into a host cell (*see Sambrook et al., supra*). It is only necessary that the particular procedure utilized be capable of successfully introducing at least one gene into the host cell which is capable of expressing the gene.

WO 00/27994

PCT/US99/26923

Any of a number of well known cells and cell lines can be used to express the polypeptides of the invention. For instance, prokaryotic cells such as *E. coli* can be used. Eukaryotic cells include, yeast, Chinese hamster ovary (CHO) cells, COS cells, and insect cells.

5           The particular vector used to transport the genetic information into the cell is also not particularly critical. Any of the conventional vectors used for expression of recombinant proteins in prokaryotic and eukaryotic cells may be used. Expression vectors for mammalian cells typically contain regulatory elements from eukaryotic viruses.

10           The expression vector typically contains a transcription unit or expression cassette that contains all the elements required for the expression of the polypeptide DNA in the host cells. A typical expression cassette contains a promoter operably linked to the DNA sequence encoding a polypeptide and signals required for efficient polyadenylation of the transcript. The term "operably linked" as used herein refers to linkage of a  
15 promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. The promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

20           Following the growth of the recombinant cells and expression of the polypeptide, the culture medium is harvested for purification of the secreted protein. The media are typically clarified by centrifugation or filtration to remove cells and cell debris and the proteins are concentrated by adsorption to any suitable resin or by use of ammonium sulfate fractionation, polyethylene glycol precipitation, or by ultrafiltration.  
25 Other routine means known in the art may be equally suitable. Further purification of the polypeptide can be accomplished by standard techniques, for example, affinity chromatography, ion exchange chromatography, sizing chromatography, His<sub>6</sub> tagging and Ni-agarose chromatography (as described in Dobeli *et al.*, *Mol. and Biochem. Parasit.* 41:259-268 (1990)), or other protein purification techniques to obtain homogeneity. The  
30 purified proteins are then used to produce pharmaceutical compositions, as described below.

An alternative method of preparing recombinant polypeptides useful as vaccines involves the use of recombinant viruses (e.g., vaccinia). Vaccinia virus is grown

WO 00/27994

PCT/US99/26923

in suitable cultured mammalian cells such as the HeLa S3 spinner cells, as described by Mackett *et al.*, in *DNA cloning Vol. II: A practical approach*, pp. 191-211 (Glover, ed.).

#### Antibody Production

The proteins of the present invention can be used to produce antibodies specifically reactive with *C pneumoniae* antigens. If isolated proteins are used, they may be recombinantly produced or isolated from *Chlamydia* cultures. Synthetic peptides made using the protein sequences may also be used.

Methods of production of polyclonal antibodies are known to those of skill in the art. In brief, an immunogen, preferably a purified protein, is mixed with an adjuvant and animals are immunized. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera is prepared. Further fractionation of the antisera to enrich for antibodies reactive to *Chlamydia* proteins can be done if desired (*see Harlow & Lane, Antibodies: A Laboratory Manual* (1988)).

Polyclonal antisera are used to identify and characterize *Chlamydia* in the tissues of patients using, for instance, *in situ* techniques and immunoperoxidase test procedures described in Anderson *et al. JAVMA* 198:241 (1991) and Barr *et al. Vet. Pathol.* 28:110-116 (1991).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol.* 6:511-519 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host.

Monoclonal antibodies produced in such a manner are used, for instance, in ELISA diagnostic tests, immunoperoxidase tests, immunohistochemical tests, for the *in vitro* evaluation of spirochete invasion, to select candidate antigens for vaccine development, protein isolation, and for screening genomic and cDNA libraries to select appropriate gene sequences.

WO 00/27994

PCT/US99/26923

Immunodiagnostic detection of *C. pneumoniae* infections

The present invention also provides methods for detecting the presence or absence of *C. pneumoniae*, or antibodies reactive with it, in a biological sample. For instance, antibodies specifically reactive with *Chlamydia* can be detected using either

5 *Chlamydia* proteins or the isolates described here. The proteins and isolates can also be used to raise specific antibodies (either monoclonal or polyclonal) to detect the antigen in a sample. In addition, the nucleic acids disclosed and claimed here can be used to detect *Chlamydia*-specific sequences using standard hybridization techniques.

For a review of immunological and immunoassay procedures in general,

10 see *Basic and Clinical Immunology* (Stites & Terr ed., 7th ed. 1991)). The immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology* (1985)). For instance, the proteins and antibodies disclosed here are conveniently used in ELISA, immunoblot analysis and

15 agglutination assays.

In brief, immunoassays to measure anti-*Chlamydia* antibodies or antigens can be either competitive or noncompetitive binding assays. In competitive binding assays, the sample analyte (e.g., anti-*Chlamydia* antibodies) competes with a labeled analyte (e.g., anti-*Chlamydia* monoclonal antibody) for specific binding sites on a capture

20 agent (e.g., isolated *Chlamydia* protein) bound to a solid surface. The concentration of labeled analyte bound to the capture agent is inversely proportional to the amount of free analyte present in the sample.

Noncompetitive assays are typically sandwich assays, in which the sample analyte is bound between two analyte-specific binding reagents. One of the binding

25 agents is used as a capture agent and is bound to a solid surface. The second binding agent is labelled and is used to measure or detect the resultant complex by visual or instrument means.

A number of combinations of capture agent and labelled binding agent can be used. For instance, an isolated *Chlamydia* protein or culture can be used as the

30 capture agent and labelled anti-human antibodies specific for the constant region of human antibodies can be used as the labelled binding agent. Goat, sheep and other non-human antibodies specific for human immunoglobulin constant regions (e.g.,  $\gamma$  or  $\mu$ ) are

WO 00/27994

PCT/US99/26923

well known in the art. Alternatively, the anti-human antibodies can be the capture agent and the antigen can be labelled.

Various components of the assay, including the antigen, anti-*Chlamydia* antibody, or anti-human antibody, may be bound to a solid surface. Many methods for  
5 immobilizing biomolecules to a variety of solid surfaces are known in the art. For instance, the solid surface may be a membrane (e.g., nitrocellulose), a microtiter dish (e.g., PVC or polystyrene) or a bead. The desired component may be covalently bound or noncovalently attached through nonspecific bonding.

Alternatively, the immunoassay may be carried out in liquid phase and a  
10 variety of separation methods may be employed to separate the bound labeled component from the unbound labelled components. These methods are known to those of skill in the art and include immunoprecipitation, column chromatography, adsorption, addition of magnetizable particles coated with a binding agent and other similar procedures.

An immunoassay may also be carried out in liquid phase without a  
15 separation procedure. Various homogeneous immunoassay methods are now being applied to immunoassays for protein analytes. In these methods, the binding of the binding agent to the analyte causes a change in the signal emitted by the label, so that binding may be measured without separating the bound from the unbound labelled component.

20 Western blot (immunoblot) analysis can also be used to detect the presence of antibodies to *Chlamydia* in the sample. This technique is a reliable method for confirming the presence of antibodies against a particular protein in the sample. The technique generally comprises separating proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a  
25 nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the separated proteins. This causes specific target antibodies present in the sample to bind their respective proteins. Target antibodies are then detected using labeled anti-human antibodies.

The immunoassay formats described above employ labelled assay  
30 components. The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. A wide variety of labels may be used. The component may be labelled by any one of several methods. Traditionally a radioactive label incorporating  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^{32}\text{P}$  was used. Non-radioactive labels



WO 00/27994

PCT/US99/26923

include ligands which bind to labelled antibodies, fluorophores, chemiluminescent agents, enzymes, and antibodies which can serve as specific binding pair members for a labelled ligand. The choice of label depends on sensitivity required, ease of conjugation with the compound, stability requirements, and available instrumentation.

5               Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labelling or  
10               signal producing systems which may be used, see U.S. Patent No. 4,391,904, which is incorporated herein by reference.

                  Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (e.g., streptavidin) molecule which is either inherently detectable or  
15               covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labelled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an  
20               antibody.

                  Some assay formats do not require the use of labelled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labelled and the presence of  
25               the target antibody is detected by simple visual inspection.

#### Pharmaceutical Compositions

                  The peptides or antibodies (typically monoclonal antibodies) of the present invention and pharmaceutical compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent *Chlamydia* infections. Suitable  
30               formulations are found in *Remington's Pharmaceutical Sciences*, Mack Publishing Company, Philadelphia, PA, 17th ed. (1985).

WO 00/27994

PCT/US99/26923

The immunogenic peptides or antibodies of the invention are administered prophylactically or to an individual already suffering from the disease. The peptide compositions are administered to a patient in an amount sufficient to elicit an effective immune response to *Chlamydia*. An effective immune response is one that inhibits infection. An amount adequate to accomplish this is defined as "therapeutically effective dose" or "immunogenically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 0.1 mg to about 1.0 mg per 70 kilogram patient, more commonly from about 0.5 mg to about 0.75 mg per 70 kg of body weight. Boosting dosages are typically from about 0.1 mg to about 0.5 mg of peptide using a boosting regimen over weeks to months depending upon the patient's response and condition. A suitable protocol would include injection at time 0, 4, 2, 6, 10 and 14 weeks, followed by further booster injections at 24 and 28 weeks.

For therapeutic use, administration should begin at the first sign of infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In some circumstances, loading doses followed by boosting doses may be required. The resulting immune response helps to cure or at least partially arrest symptoms and/or complications. Vaccine compositions containing the peptides are administered prophylactically to a patient susceptible to or otherwise at risk of the infection.

The pharmaceutical compositions (containing either peptides or antibodies) are intended for parenteral or oral administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic polypeptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.4% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain

WO 00/27994

PCT/US99/26923

pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

5           The compositions may also comprise carriers to enhance the immune response. Useful carriers are well known in the art, and include, e.g., KLH, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like.

10           For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as  
15 those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

As noted above, the peptide compositions are intended to induce an immune response to *Chlamydia*. Thus, compositions and methods of administration suitable for maximizing the immune response are preferred. For instance, peptides may  
20 be introduced into a host, including humans, linked to a carrier or as a homopolymer or heteropolymer of active peptide units from various *Chlamydia* proteins disclosed here. Alternatively, a "cocktail" of polypeptides can be used. A mixture of more than one polypeptide has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies to a  
25 number of epitopes.

The compositions also include an adjuvant. As used here, number of adjuvants are well known to one skilled in the art. Suitable adjuvants include incomplete Freund's adjuvant, alum, aluminum phosphate, aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP),  
30 N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl

WO 00/27994

PCT/US99/26923

lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion. The effectiveness of an adjuvant may be determined by measuring the amount of antibodies directed against the immunogenic peptide.

5 The concentration of immunogenic peptides of the invention in the pharmaceutical formulations can vary widely, i.e. from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

10 The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector  
15 is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (*Nature* 351:456-460 (1991)). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g., *Salmonella typhi* vectors and the like, will be apparent to those skilled in the art from the description herein.

20 The DNA encoding one or more of the peptides of the invention can also be administered to the patient. This approach is described, for instance, in Wolff et al., *Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466.

In order to enhance serum half-life, the peptides may also be encapsulated, introduced into the lumen of liposomes, prepared as a colloid, or other conventional  
25 techniques may be employed which provide an extended serum half-life of the peptides. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), U.S. Pat. Nos. 4,235,871, 4,501,728 and 4,837,028.

30

### EXAMPLES

The following examples are offered to illustrate, but no to limit the claimed invention.

#### Example 1:

WO 00/27994

PCT/US99/26923

This example describes comparison of the *C. pneumoniae* genome disclosed here and the, previously sequenced, *C. trachomatis* genome (Stephens, *et al. Science* 282:754-759 (1998)).

The apparent low level of DNA homology between *C. trachomatis* and *C. pneumoniae* (Campbell, *et al., J. Clin. Microbiol.* 25:1911-1916 (1987)) yet analogous cell structures and developmental cycles, predicts that comparative analysis of the two genomes will significantly enhance the understanding of both pathogens. Identification of genes that are present in one species but not the other are of particular importance for the mutually exclusive biological, virulence and pathogenesis capabilities of each.

Identification of genes shared between the two species strongly supports the requirement for these capabilities in a biological system that has, over its long-term association with mammalian host cells, evolved to reduce the metabolic capacities while optimizing survival, growth and transmission of these unique pathogens.

The previously sequenced *C. trachomatis* genome contains 1,042,519 nucleotides and 875 likely protein-coding genes. Similarity searching permitted the inferred functional assignment of sequences 636 (60%) genes disclosed here and 251 (23%) are similar to hypothetical genes for other bacterial organisms including those for *C. trachomatis*. The remaining 186 (17%) genes are not homologous to sequences deposited in GenBank.. Seventy *C. trachomatis* genes are not represented in the *C. pneumoniae* genome. These are contained within blocks consisting of 2-17 genes and 19 single genes. Of the 70 *C. trachomatis* genes without homologs in *C. pneumoniae*, 60 are classified as encoding hypothetical proteins. The remaining genes not represented in *C. pneumoniae* consist of the tryptophan operon (*trpA,B,R*), *trpC*, two predicted thiol protease genes, and 4 genes assigned to the phospholipase-D superfamily.

It is evident that there is a high level of functional conservation between *C. pneumoniae* and *C. trachomatis* as orthologs to *C. trachomatis* genes were identified for 859 (80%) of the predicted coding sequences for *C. pneumoniae*. The level of similarity for individual encoded proteins spans a wide spectrum (22-95% amino acid identity) with an average of 62% amino acid identity between orthologs from the two species. The percent amino acid identity between orthologous chlamydial proteins is similar among functional groups with the highest for proteins associated with translation and the lowest for proteins whose function in chlamydiae is uncharacterized and not related to proteins encoded by other organisms. The gene order of the homologous set of genes in *C.*

WO 00/27994

PCT/US99/26923

*pneumoniae* shows reorganization relative to the genome of *C. trachomatis*; however, there is a high level of synteny for the gene organization of the two genomes. We identified thirty-nine blocks of 2 or more genes whose gene organization is colinear with homologs to *C. trachomatis*, although some of these are inverted. The distribution of genome reorganization is not evenly distributed on the chromosome as the region between *C. pneumoniae* coding sequences 0130-0300 contains substantially more reorganization than other areas of the genome. This region coincides with the predicted chromosome replication terminus.

We identified orthologs of enzymes characterized in other bacteria that account for the essential requirements for DNA replication, repair, transcription and translation including two predicted DNA helicases of the Swi2/Snf2 family found in *C. trachomatis*. Similar to *C. trachomatis*, alternative sigma subunits for RNA polymerase,  $\sigma^{28}$  and  $\sigma^{54}$ , were identified in addition to anti- $\sigma$  regulatory system factors RsbV, a RsbW-like single-domain histidine kinase, and a RsbU-like protein phosphatase. These findings suggest that the fundamental mechanisms of transcriptional regulation are conserved among *Chlamydia*. The *C. trachomatis* proteins containing SET and SWIB domains, and a SWIB domain fused to the C-terminus of the chlamydial topoisomerase I, not identified outside eukaryotes, are found in *C. pneumoniae* supporting their possible role in the chromatin condensation-decondensation characteristic of the biologically unique chlamydial developmental cycle.

The central metabolic pathways inferred from the *C. pneumoniae* genome sequence are the same as those identified for *C. trachomatis*. *C. pneumoniae* has a glycolytic pathway and a linked tricarboxylic acid cycle, although likely functional, is incomplete as genes for citrate synthase, aconitase, and isocitrate dehydrogenase were not identified. *C. pneumoniae* has a complete glycogen synthesis and degradation system supporting a role for glycogen synthesis and utilization of glucose-derivatives in chlamydial metabolism. Genes encoding essential functions in aerobic respiration are present and electron flux may be supported by pyruvate, succinate, glycerol-3-phosphate, and NADH dehydrogenases, NADH-ubiquinone oxidoreductase and cytochrome oxidase. *C. pneumoniae* also contains the V (vacuolar)-type ATPase operon and the two ATP translocases found in *C. trachomatis*.

The type-III secretion virulence system required for invasion by several pathogenic bacteria and found in the *C. trachomatis* genome in three chromosomal

WO 00/27994

PCT/US99/26923

locations is also present in the *C. pneumoniae* genome. Each of the components is conserved and their relative genomic contexts are conserved. Genes such as a predicted serine/threonine protein kinase and other genes physically linked to genes encoding structural components of the type-III secretion apparatus, but without identified  
5 homologs, are also highly similar between the two species suggesting the functional roles in modifying cellular biology are fundamentally conserved.

*Chlamydia*-encoded proteins that are not found in chlamydial organisms but localized to the intracellular chlamydial inclusion membrane are likely essential for the unique intracellular biology and perhaps differences in inclusion morphology  
10 observed between species of *Chlamydia*. Several such proteins, termed IncA, B & C, have been characterized for a *C. psittaci* strain (Rockey, et al. *Mol. Microbiol.* 15:617-626 (1995); Rockey et al. *Infect. Immun.* 62:106-112 (1994)). *C. pneumoniae* and *C. trachomatis* encode orthologs to *C. psittaci* IncB and IncC and *C. trachomatis* also contains an ortholog to IncA. *C. pneumoniae* contains two genes that encode proteins  
15 with similarity to IncA (CPn0186 and CPn0585), although the level of homology is low suggesting analogous but possibly altered functions.

The tryptophan biosynthesis operon (*trpA*, *trpB*, *trpR*) and *trpC* identified in *C. trachomatis* is conspicuously missing in the *C. pneumoniae* genome. This represents the entire repertoire of genes associated with tryptophan biosynthesis identified  
20 in *C. trachomatis*. Seventeen genes adjacent to the *C. trachomatis* tryptophan operon also were not found in the *C. pneumoniae* genome. This region is the single largest loss of a contiguous genomic segment and includes 4 HKD superfamily encoding genes that encompass a family of proteins related to endonuclease and phospholipase D. These findings may be important for the ability of *Chlamydia* to persist in their hosts and cause  
25 disease by eliciting potent, focal and persistent inflammatory responses thought to be essential for pathogenesis.

The *C. pneumoniae* genome contains 187,711 additional nucleotides compared to the *C. trachomatis* genome, and the 214 coding sequences not found in *C. trachomatis* account for most of the increased genome size. Eighty-eight of these genes  
30 are found in blocks of >10 genes (11-30 genes/block), 41 are single genes, and the remainder are partnered with at least one other gene. Based upon the observation that ~70% of all the *C. pneumoniae* genes have an identifiable homolog in GenBank, exclusive of *C. trachomatis*, it would be expected that over 150 of the 214 genes should

WO 00/27994

PCT/US99/26923

have a homolog in GenBank, many associated with a function. However, only 28 coding sequences have similarity to genes from other organisms. Thus the majority of the genes that are mutually exclusive of *C. trachomatis* (186 of 214), and the 60 of 70 *C. trachomatis* genes that lacked an identifiable homolog in *C. pneumoniae*, do not have detectable homologs to genes from other organisms. We predict that most of the unique genes are essential for specific attributes that define the differential biology, tropism and pathogenesis of *C. trachomatis* and *C. pneumoniae*. Moreover, this suggests that *C. pneumoniae* has more unique biological (i.e., virulence) capacity than *C. trachomatis*. The ability of *C. pneumoniae* to be more invasive and survive in a broader range of host cell types than *C. trachomatis* is consistent with this hypothesis. Not all of the differences in biological capacity may be associated with mutually exclusive genes. One explanation for the significantly lower level of homology between protein sequences assigned as having *C. pneumoniae* and *C. trachomatis* orthologs but no identifiable orthologs in other organisms is that this set of proteins is not only associated with biological requirements specific for *Chlamydia* but this polymorphism may account for differential biology between the two species. The determination of the genome sequence from a representative of the *C. psittaci* group will precisely delineate those genes that are mutually exclusive and specific for each species.

The major functionally identifiable addition to the *C. pneumoniae* genome is a large expansion of genes encoding a new family of chlamydial polymorphic membrane proteins (Pmp), alone representing 22% of the increased coding capacity. While the *C. trachomatis* genome has 9 *pmp* genes, remarkably the *C. pneumoniae* genome contains 21 *pmp* genes. Most of these genes appear to be amplified in two regions of the genome with three stand-alone genes. Interestingly one of the stand-alone genes is most closely related to the *C. trachomatis pmpD* which is the only stand-alone *pmp* gene in the *C. trachomatis* genome and it is located with the same relative genomic context, suggesting an essential and conserved function for this paralog. Six Pmp-coding genes are presumably not functional as five contain predicted coding frame-shifts and one is truncated. The amplification of this gene family and the confidently predicted frame-shifts suggest a specific molecular mechanism to promote functional or antigenic diversity. The biological role of this protein family remains enigmatic, although at least one of the proteins in *C. psittaci* related to this family is exposed on the chlamydial surface.



WO 00/27994

PCT/US99/26923

While a function could not be assigned for most of the unique *C. pneumoniae* genes, several have significant similarity to genes from other organisms. Functional assignments could be made for genes encoding GMP synthetase, IMP dehydrogenase, UMP synthase, uridine kinase, biotin synthase pathway proteins, methylthioadenosine nucleosidase, a DNA glycosylase and aromatic amino acid hydroxylase. Thus a complete pathway was identified for biotin biosynthesis. The additional purine and pyrimidine salvage pathway genes presumably reflect metabolic limitations in one of the cell types that *C. pneumoniae* infects or differences in the ability of *C. pneumoniae* to transport precursor nucleosides or nucleotides.

The addition of aromatic amino acid hydroxylase in *C. pneumoniae* is intriguing especially in light of the loss of tryptophan biosynthetic genes and the inability to synthesize other amino acids including phenylalanine. Aromatic amino acid hydroxylases include three distinct enzymes that function to receptively oxidize phenylalanine to tyrosine, tyrosine to Dopa, and tryptophan to 5-hydroxytryptophan and serotonin. Although the chlamydial protein is similar to proteins of this family and incrementally more closely related to tryptophan hydroxylase, its specific function could not be confidently predicted. We hypothesize that it may be involved in *C. pneumoniae* virulence. Tryptophan hydroxylase has not been previously identified in bacteria and the origin of the chlamydial gene appears to be from eukaryotes. The functional role of an aromatic amino acid hydroxylase for *C. pneumoniae* is linked to the unique intracellular biology of this organism and may represent a key contribution to *C. pneumoniae* persistence and pathogenesis.

It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

Table 1 provides functional assignments of *C. pneumoniae* nonprotein-encoding genomic sequences. Table 2 provides functional assignments of protein coding sequences. Table 3 provides the amino acid sequences of the proteins corresponding to the coding sequences.

WO 00/27994

PCT/US99/26923

TABLE 1

type	SEQ ID NO:1 start position	SEQ ID NO:1 end position	Gene
Ori	841664	841396	(R) Putative Origin of Replica
tmRNA	138493	138074	(R) tmRNA
pRNA	607342	607649	Ribonuclease P RNA
rRNA	1000564	1002115	16S rRNA
rRNA	1002415	1005278	23S rRNA
rRNA	1005393	1005509	5S rRNA
tRNA	269070	269142	Ala tRNA <sub>1</sub>
tRNA	164318	164389	Asn tRNA
tRNA	296224	296151	(R) Asp tRNA
tRNA	836191	836119	(R) Ala tRNA <sub>2</sub>
tRNA	1030533	1030603	Cys tRNA
tRNA	784896	784822	(R) Glu tRNA
tRNA	781680	781610	(R) Gly tRNA <sub>1</sub>
tRNA	961536	961607	Gly tRNA <sub>2</sub>
tRNA	999949	1000023	His tRNA
tRNA	268992	269065	Ile tRNA
tRNA	672236	672318	Leu tRNA <sub>1</sub>
tRNA	680178	680257	Leu tRNA <sub>2</sub>
tRNA	715889	715971	Leu tRNA <sub>3</sub>
tRNA	739403	739486	Leu tRNA <sub>4</sub>
tRNA	1175863	1175944	Leu tRNA <sub>5</sub>
tRNA	784994	784922	(R) Lys tRNA
tRNA	843926	843999	Pro tRNA <sub>2</sub>
tRNA	409922	409848	(R) Pro tRNA <sub>1</sub>
tRNA	631373	631445	Phe tRNA
tRNA	677337	677264	(R) Arg tRNA <sub>2</sub>
tRNA	807413	807341	(R) Arg tRNA <sub>3</sub>
tRNA	877473	877400	(R) Arg tRNA <sub>4</sub>
tRNA	462141	462214	Arg tRNA <sub>1</sub>
tRNA	1085605	1085676	Gln tRNA
tRNA	786780	786708	(R) Thr tRNA <sub>3</sub>
tRNA	89728	89657	(R) Thr tRNA <sub>1</sub>
tRNA	293477	293405	(R) Thr tRNA <sub>2</sub>
tRNA	87522	87450	(R) Met tRNA <sub>1</sub>
tRNA	199301	199229	(R) Met tRNA <sub>2</sub>
tRNA	199390	199317	(R) Met tRNA <sub>3</sub>
tRNA	626904	626987	Ser tRNA <sub>1</sub>
tRNA	708359	708440	Ser tRNA <sub>2</sub>
tRNA	1142034	1142117	Ser tRNA <sub>3</sub>
tRNA	1230028	1229945	(R) Ser tRNA <sub>4</sub>
tRNA	91070	90999	(R) Trp tRNA
tRNA	293399	293317	(R) Tyr tRNA
tRNA	296147	296075	(R) Val tRNA <sub>1</sub>
tRNA	1137389	1137462	Val tRNA <sub>2</sub>

WO 00/27994

PCT/US99/26923

TABLE 2

Gene	From	To	Strand	Gene Function (C. trachomatis ortholog in parentheses)
CPn0001	282	4	R	CT001 hypothetical protein
CPn0002	571	875	F	gatC-Glu-tRNA Gln Amidotransferase (C subunit)-(CT002)
CPn0003	895	2370	F	gatA-Glu tRNA Gln Amidotransferase-(CT003)
CPn0004	3170	3111	F	gatB-(Pct113) Glu tRNA Gln Amidotransferase (B subunit)-(CT004)
CPn0005	4127	6492	F	pmp_1-Polymorphic Outer Membrane Protein G Family
CPn0006	7293	7141	R	
CPn0007	7605	10496	F	
CPn0008	10975	11685	F	
CPn0009	11815	13119	F	
CPn0010	13435	14325	F	
CPn0010	14379	15746	F	frame-shift with 0010
CPn0011	15892	16614	F	
CPn0012	16644	18212	F	
CPn0013	18584	21106	F	pmp_2-Polymorphic Outer Membrane Protein G Family
CPn0014	21392	21922	F	pmp_3-Polymorphic Outer Membrane Protein G Family
CPn0015	21835	24174	F	pmp_3-PMP_3 (frame-shift with 0014)
CPn0016	24416	26188	F	pmp_4-Polymorphic Outer Membrane Protein G Family
CPn0017	26094	27170	F	pmp_4-PMP_4 (frame-shift with 0016)
CPn0018	27522	29003	F	pmp_5-Polymorphic Outer Membrane Protein G Family
CPn0019	29007	30356	F	pmp_5-PMP_5 (frame-shift with 0018)
CPn0020	32687	30603	R	Predicted OMP (leader (14) peptide: outer membrane)-(CT351)
CPn0021	34410	32707	R	Predicted OMP (leader (19) peptide)-(CT350)
CPn0022	34982	34395	R	maf-(CT349)
CPn0023	36603	35014	R	yjyK/atr-ABC Transporter Protein ATPase-(CT348)
CPn0024	37596	36661	F	xerC-Integrase/recombinase-(CT347)
CPn0025	38604	37684	R	elaC/ataA-Sulphohydrolase/Glycosulfatase-(CT346)
CPn0026	39625	38762	R	CT345 hypothetical protein-(CT345)
CPn0027	42234	39778	R	lon-Lon ATP-dependent Protease-(CT344)
CPn0028	43325	42543	R	
CPn0029	43755	43390	R	
CPn0030	43891	44529	F	gcp_1-O-Sialoglycoprotein Endopeptidase_1-(CT343)
CPn0031	44711	44884	F	rs21-S21 Ribosomal Protein-(CT342)
CPn0032	44923	46098	F	dnaJ-Heat Shock Protein J-(CT341)
CPn0033	46138	48171	F	pdhAAB/odhAodhB-(pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta Fusion-(CT340)
CPn0034	49457	48210	R	
CPn0035	51029	49569	R	CT339 hypothetical protein
CPn0036	51002	51796	F	CT338 hypothetical protein
CPn0037	51792	52115	F	ptsH-PTS Phosphocarrier Protein Hpr-(CT337)
CPn0038	52119	53831	F	ptsI-PTS PEP Phosphotransferase-(CT336)
CPn0039	54250	53963	R	ybaB-(CT335)
CPn0040	55643	54318	R	dnaX_1-DNA Pol III Gamma and Tau_1-(CT334)
CPn0041	55996	57342	F	
CPn0042	57403	58182	F	
CPn0043	58447	60372	F	
CPn0044	60419	60778	F	
CPn0045	61069	62790	F	
CPn0046	62790	63263	F	
CPn0047	63455	63652	F	
CPn0048	63687	65801	F	*yqfP-Bs conserved hypothetical IM protein
CPn0049	66296	65817	R	
CPn0050	66813	66499	R	
CPn0051	66833	67111	F	
CPn0052	68005	67304	R	hemC-Porphobilinogen Deaminase-(CT299)
CPn0053	69344	67986	R	sms-Sms Protein-(CT298)
CPn0054	70023	69313	R	rnc-Ribonuclease III-(CT297)
CPn0055	70129	70590	F	CT296 hypothetical protein
CPn0056	70953	72746	F	msrA-Phosphomannomutase-(CT295)
CPn0057	72934	73554	F	sodM-Superoxide Dismutase (Mn)-(CT294)
CPn0058	73639	74562	F	accD-AcCoA Carboxylase/Transferase Beta-(CT293)
CPn0059	74616	75050	F	duc-dUTP Nucleotidohydrolase-(CT292)
CPn0060	75055	75528	F	ptsN_1-PTS IIA Protein-(CT291)
CPn0061	75534	76208	F	ptsN_2-PTS IIA Protein + HTH DNA-Binding Domain-(CT290)
CPn0062	76308	77490	F	CT289 hypothetical protein
CPn0063	78112	78267	F	
CPn0064	78346	78576	F	
CPn0065	78924	80651	F	CT288 hypothetical protein
CPn0066	80925	82655	F	

WO 00/27994

PCT/US99/26923

CPn0067	82953	84053	F	
CPn0068	84903	84331	R	CT360 hypothetical protein
CPn0069	85236	87086	F	
CPn0070	87378	87208	R	
CPn0071	88045	87599	R	CT325 hypothetical protein
CPn0072	89061	88057	R	CT324 hypothetical protein
CPn0073	89356	89574	F	infA-Initiation Factor IF-1-(CT323)
CPn0074	89774	90955	F	tufA-Elongation Factor Tu-(CT322)
CPn0075	91102	91350	F	secE-preprotein translocase-(CT321)
CPn0076	91358	91903	F	nusG-Transcriptional Antitermination-(CT320)
CPn0077	92013	92435	F	rll1-L11 Ribosomal Protein-(CT319)
CPn0078	92465	93160	F	rll1-L1 Ribosomal Protein-(CT318)
CPn0079	93179	93688	F	rll0-L10 Ribosomal Protein-(CT317)
CPn0080	93735	94121	F	r17-L7/L12 Ribosomal Protein-(CT316)
CPn0081	94261	98016	F	rpoB-RNA Polymerase Beta-(CT315)
CPn0082	98043	102221	F	rpoC-RNA Polymerase Beta' -(CT314)
CPn0083	102332	103312	F	tal-Transaldolase-(CT313)
CPn0084	103362	103751	F	predicted ferredoxin-(CT312)
CPn0085	104506	103766	R	CT311 hypothetical protein
CPn0086	104904	105527	F	atpE-ATP Synthase Subunit E-(CT310)
CPn0087	105579	106376	F	CT309 hypothetical protein
CPn0088	106373	108145	F	atpA-ATP Synthase Subunit A-(CT308)
CPn0089	108153	109466	F	atpB-ATP Synthase Subunit B-(CT307)
CPn0090	109454	110080	F	atpD-ATP Synthase Subunit D-(CT306)
CPn0091	110074	112053	F	atpI-ATP Synthase Subunit I-(CT305)
CPn0092	112151	112573	F	atpK-ATP Synthase Subunit K-(CT304)
CPn0093	112509	113015	F	CT303 hypothetical protein
CPn0094	113152	115971	F	valS-Valyl tRNA Synthetase-(CT302)
CPn0095	116037	118790	F	pknD-S/T Protein Kinase-(CT301)
CPn0096	124314	118837	R	uvrA-Excinuclease ABC Subunit A-(CT333)
CPn0097	124555	126006	F	pyk-Pyruvate Kinase-(CT332)
CPn0098	127491	126091	R	htrB-Acyltransferase-(CT010)
CPn0099	127593	127865	F	
CPn0100	129141	127882	R	CT011 hypothetical protein
CPn0101	129932	129141	R	ybbP family hypothetical protein-(CT012)
CPn0102	130123	131466	F	cydA-Cytochrome Oxidase Subunit I-(CT013)
CPn0103	131480	132511	F	cydB-Cytochrome Oxidase Subunit II-(CT014)
CPn0104	133875	132676	R	CT017 hypothetical protein
CPn0105	134847	134029	R	CT016 hypothetical protein
CPn0106	135091	136374	F	phoH-ATPase-(CT015)
CPn0107	137162	136392	R	CT058 hypothetical protein_1
CPn0108	137857	137303	R	CT018
CPn0109	138655	141783	F	ileS-Isoleucyl-tRNA Synthetase-(CT019)
CPn0110	143734	141827	R	lepB-Signal Peptidase I-(CT020)
CPn0111	144686	143934	R	CT021 hypothetical protein
CPn0112	144767	145093	F	rll3-L31 Ribosomal Protein-(CT022)
CPn0113	145335	146405	F	pfrA-Peptide Chain Releasing Factor (RF-1)-(CT023)
CPn0114	146398	147261	F	hemK-A/G specific methylase-(CT024)
CPn0115	147279	148622	F	ffh-Signal Recognition Particle GTPase-(CT025)
CPn0116	148616	148972	F	rs16-S16 Ribosomal Protein-(CT026)
CPn0117	148989	150071	F	trmD-tRNA (guanine N-1)-Methyltransferase-(CT027)
CPn0118	150102	150464	F	rll9-L19 Ribosomal Protein-(CT028)
CPn0119	150523	151164	F	rnhB_1-Ribonuclease HII_1-(CT029)
CPn0120	151164	151778	F	gmK-GMP Kinase-(CT030)
CPn0121	151778	152068	F	CT031 hypothetical protein
CPn0122	152071	153723	F	metG-Methionyl-tRNA Synthetase-(CT032)
CPn0123	155969	153774	R	recD_1-Exodeoxyribonuclease V (Alpha Subunit)_1-(CT033)
CPn0124	156614	158068	F	
CPn0125	158096	158605	F	
CPn0126	158809	161085	F	
CPn0127	162143	161130	R	ytjF-Cationic Amino Acid Transporter-(CT034)
CPn0128	162277	163053	F	bpl1-Biotin Protein Ligase-(CT035)
CPn0129	163717	163064	R	similarity to CT036
CPn0130	164245	163751	R	
CPn0131	164549	165580	F	
CPn0132	165587	166561	F	
CPn0133	167334	166564	R	CHLPS hypothetical protein-(CT109)
CPn0134	169098	167467	R	groEL_1-HSP-60_1-(CT110)
CPn0135	169448	169143	R	groES-10KDa Chaperonin-(CT111)
CPn0136	171401	169569	R	pepF-Oligopeptidase-(CT112)
CPn0137	172254	171502	R	ybgI-ACR family-(CT108)
CPn0138	174019	172700	R	hemL-Glutamate-1-semialdehyde-2,1-aminomutase-(CT210)

WO 00/27994

PCT/US99/26923

CPn0139	174656	174093	R	yqqE-(CT210)
CPn0140	175110	174673	R	yqkE-(CT212)
CPn0141	175802	175110	R	rpiA-Ribose-5-P Isomerase A-(CT213)
CPn0142	176091	175816	R	
CPn0143	177335	176214	R	*YKJG_Bs_1 Hypothetical Protein
CPn0144	177963	180560	F	clpB-Clp Protease ATPase-(CT113)
CPn0145	180777	182369	F	CT114 hypothetical protein
CPn0146	182613	183095	F	
CPn0147	183225	183671	F	
CPn0148	183846	185702	F	pknI-S/T Protein Kinase-(CT145)
CPn0149	185715	187700	F	dnlJ-DNA Ligase-(CT146)
CPn0150	187834	192444	F	CT147 hypothetical protein
CPn0151	194142	192625	R	mhpA-Monooxygenase-(CT148)
CPn0152	195265	194318	R	CT149 hypothetical protein
CPn0153	195433	197892	F	leuS-Leucyl tRNA Synthetase-(CT209)
CPn0154	197892	199202	F	gsea-KDO Transferase-(CT208)
CPn0155	199691	199488	R	
CPn0156	200117	199770	R	
CPn0157	200723	200298	R	
CPn0158	201430	200894	R	
CPn0159	201772	201467	R	
CPn0160	203791	202127	R	pfkA_1-Fructose-6-P Phosphotransferase_1-(CT207)
CPn0161	204622	203798	R	predicted acyltransferase family-(CT206)
CPn0162	205828	204803	R	
CPn0163	206026	206394	F	
CPn0164	206498	206998	F	
CPn0165	206998	207582	F	
CPn0166	207630	207962	F	
CPn0167	208306	207977	R	
CPn0168	208641	208417	R	
CPn0169	209501	208710	R	
CPn0170	211026	210025	R	
CPn0171	212435	211149	R	*guaA-GMP Synthase
CPn0172	213177	212440	R	*guaB/impD-Inosine 5'-monophosphate dehydrogenase (COOH-terminal region only)
CPn0173	213987	213715	R	
CPn0174	214257	214724	F	
CPn0175	214898	215275	F	
CPn0176	215286	216518	F	CT153 hypothetical protein
CPn0177	217459	216608	R	
CPn0178	218052	217789	R	
CPn0179	218403	218056	R	
CPn0180	218851	218355	R	
CPn0181	219175	218777	R	
CPn0182	220695	219334	R	accC-Biotin Carboxylase-(CT124)
CPn0183	221195	220695	R	accB-Biotin Carboxyl Carrier Protein-(CT123)
CPn0184	221775	221221	R	efp_1-Elongation Factor P_1-(CT122)
CPn0185	222451	221765	R	rpe/araD-Ribulose-5-P Epimerase-(CT121)
CPn0186	222899	224068	F	*similarity to Cps IncA_1-(CT119)
CPn0187	224248	225045	F	predicted methylase-(CT133)
CPn0188	225111	226400	F	CT132 hypothetical protein
CPn0189	226400	229825	F	CT131 homolog-(Possible Transmembrane Protein)
CPn0190	229919	231274	F	
CPn0191	231991	231314	R	glnQ-ABC Amino Acid Transporter ATPase-(CT130)
CPn0192	232634	231984	R	glnP-ABC Amino Acid Transporter Permease-(CT129)
CPn0193	233126	232686	R	*argR-Arginine Repressor
CPn0194	233210	234241	F	gcp_2-O-Sialoglycoprotein Endopeptidase_2-(CT197)
CPn0195	234190	235785	F	oppA_1-Oligopeptide Binding Protein_1
CPn0196	235939	237519	F	oppA_2-Oligopeptide Binding Protein_2-(CT198)
CPn0197	237578	238882	F	oppA_3-Oligopeptide Binding Protein_3
CPn0198	239169	240746	F	oppA_4-Oligopeptide Binding Protein_4
CPn0199	241042	241983	F	oppB_1-Oligopeptide Permease_1-(CT199)
CPn0200	242017	242868	F	oppC_1-Oligopeptide Permease_1-(CT200)
CPn0201	242864	243715	F	oppD-Oligopeptide Transport ATPase-(CT201)
CPn0202	243715	244500	F	oppF-Oligopeptide Transport ATPase-(CT202)
CPn0203	245008	245802	F	
CPn0204	245817	246002	F	
CPn0205	246133	246327	F	
CPn0206	246409	247161	F	CT203 hypothetical protein
CPn0207	247208	248617	F	ybhI/sodiT1-Oxoglutarate/Malate Translocator-(CT204)
CPn0208	248953	250602	F	pfkA_2-Fructose-6-P Phosphotransferase_2-(CT205)
CPn0209	251036	251272	F	

WO 00/27994

PCT/US99/26923

CPn0210	252384	251440	R	
CPn0211	252756	252463	R	
CPn0212	254066	252888	R	
CPn0213	254342	254190	R	
CPn0214	255657	254446	R	
CPn0215	257015	255759	R	
CPn0216	257608	257174	R	
CPn0217	257896	258579	F	ypdP-(CT140)
CPn0218	259058	258582	R	
CPn0219	259357	260472	F	tgt-Queuine tRNA Ribosyl Transferase-(CT193)
CPn0220	260696	261238	F	
CPn0221	261657	262064	F	
CPn0222	262504	262842	F	*weak similarity to Bacteriophage CHP1 (Orf4)
CPn0223	262956	263333	F	
CPn0224	263435	263674	F	
CPn0225	263873	264541	F	
CPn0226	264566	264967	F	
CPn0227	265416	265009	R	dsbB-Disulfide bond Oxidoreductase-(CT176)
CPn0228	266110	265412	R	dsbG-Disulfide Bond Chaperone-(CT177)
CPn0229	266328	267560	F	CT178 hypothetical protein
CPn0230	268253	267576	R	CT179 hypothetical protein
CPn0231	268957	268253	R	tauB-ABC Transport ATPase (Nitrate/Fe)-(CT180)
CPn0232	270122	269232	R	*similarity to 5'-Methylthioadenosine / S-Adenosylhomocysteine Nucleosidase
CPn0233	270424	270248	R	
CPn0234	271240	270548	R	CT181 hypothetical protein
CPn0235	271416	272177	F	kdsB-deoxyoctulononic Acid Synthetase-(CT182)
CPn0236	272156	273766	F	pyrG-CTP Synthetase-(CT183)
CPn0237	273762	274214	F	yggF Family-(CT184)
CPn0238	274303	275838	F	zwf-Glucose-6-P Dehydrogenase-(CT185)
CPn0239	275899	276672	F	devB-Glucose-6-P Dehydrogenase (DevB family)-(CT186)
CPn0240	277861	276698	R	
CPn0241	279354	278203	R	
CPn0242	279918	279487	R	
CPn0243	280555	280133	R	
CPn0244	280918	281556	F	adk-Adenylate Kinase-(CT128)
CPn0245	281645	282499	F	ydhO-Polysaccharide Hydrolase-Invasin Repeat Family-(CT127)
CPn0246	282952	282551	R	rs9-S9 Ribosomal Protein-(CT126)
CPn0247	283415	282969	R	rl13-L13 Ribosomal Protein-(CT125)
CPn0248	284327	283650	R	ycfV/ybba-ABC Transporter ATPase-(CT152)
CPn0249	285841	284333	R	CT151 hypothetical protein
CPn0250	286057	285902	R	rl33-L33 Ribosomal Protein-(CT150)
CPn0251	286060	287559	F	*conserved hypothetical protein
CPn0252	288112	287576	R	CT144 hypothetical protein (frame-shift with 0253?)
CPn0253	288456	287950	R	CT144 hypothetical protein_1
CPn0254	289262	288459	R	CT143 hypothetical protein_1
CPn0255	290165	289329	R	CT142 hypothetical protein_1
CPn0256	291264	290398	R	CT144 hypothetical protein_2
CPn0257	292127	291267	R	CT143 hypothetical protein_2
CPn0258	292534	292133	R	CT142 hypothetical protein (frame-shift with 0259?)
CPn0259	292986	292441	R	CT142 hypothetical protein_2
CPn0260	294045	293548	R	secA_1-Protein Translocase Subunit_1-(CT141)
CPn0261	294302	295033	F	ydaO-PP-Loop Superfamily ATPase-(CT217)
CPn0262	295091	295933	F	surE-SurE-like Acid Phosphatase-(CT218)
CPn0263	296249	297136	F	yqfU hypothetical protein-(CT221)
CPn0264	297730	297155	R	ubiD-Phenylacrylate Decarboxylase-(CT220)
CPn0265	298620	297730	R	ubiA-Benzoate Octaphenyltransferase-(CT219)
CPn0266	299184	299876	F	
CPn0267	300122	300910	F	
CPn0268	300935	301318	F	
CPn0269	302450	301476	R	Dipeptidase-(CT138)
CPn0270	303325	302468	R	ywlc-SuA5 Superfamily-related Protein-(CT137)
CPn0271	303634	304362	F	Lysophospholipase esterase-(CT136)
CPn0272	305233	304340	R	dnaX_2-DNA Pol III Gamma and Tau_2-(CT187)
CPn0273	305844	305227	R	tdk-Thymidylate Kinase-(CT188)
CPn0274	308353	305852	R	gyrA_1-DNA Gyrase Subunit A_1-(CT189)
CPn0275	310786	308372	R	gyrB_1-DNA Gyrase Subunit B_1-(CT190)
CPn0276	311137	310793	R	CT191 hypothetical protein
CPn0277	311910	311404	R	
CPn0278	312875	312060	R	*conserved outer membrane lipoprotein protein
CPn0279	313537	312875	R	*Possible ABC Transporter Permease Protein
CPn0280	314572	313550	R	dppF-Dipeptide Transporter ATPase-(CT689)

WO 00/27994

PCT/US99/26923

CPn0281	315057	316103	F	dhna-Predicted 1.6-Fructose Biphosphate Aldolase (dehydrin family)-(CT215)
CPn0282	316126	317529	F	xasA/gadC-Amino Acid Transporter-(CT216)
CPn0283	318497	317532	R	
CPn0284	319045	318551	R	
CPn0285	320595	319051	R	
CPn0286	322059	320650	R	mgE-Mg-- Transporter (CBS Domain)-(CT194)
CPn0287	324221	322089	R	
CPn0288	325716	324571	R	CT195 hypothetical protein
CPn0289	325812	326996	F	aaAT-Neutral Amino Acid (Glutamate) Transporter-(CT230)
CPn0290	327042	328523	F	Na-dependent Transporter-(CT231)
CPn0291	328667	329194	F	incB-Inclusion Membrane Protein B-(CT232)
CPn0292	329228	329836	F	incC-Inclusion Membrane Protein C-(CT233)
CPn0293	329949	332723	F	CT234 hypothetical protein
CPn0294	333092	333502	F	cAMP-Dependent Protein Kinase Regulatory Subunit-(CT235)
CPn0295	333863	333627	R	acpP-Acyl Carrier Protein-(CT236)
CPn0296	334765	334022	R	fabG-Oxoacyl (Carrier Protein) Reductase-(CT237)
CPn0297	335697	334774	R	fabD-Malonyl Acyl Carrier Transcyclase-(CT238)
CPn0298	336721	335717	R	fabH-Oxoacyl Carrier Protein Synthase III-(CT239)
CPn0299	336816	337415	F	recR-Recombination Protein-(CT240)
CPn0300	337783	340152	F	yaeT-Omp85 Analog-(CT241)
CPn0301	340250	340762	F	(OmpH-Like Outer Membrane Protein)-(CT242)
CPn0302	340787	341866	F	lpxD-UDP Glucosamine N-Acyltransferase-(CT243)
CPn0303	342958	341921	F	CT244 hypothetical protein
CPn0304	343133	344158	F	pdhA/odpA-Pyruvate Dehydrogenase Alpha-(CT245)
CPn0305	344154	345137	F	pdhB/odpB-Pyruvate Dehydrogenase Beta-(CT246)
CPn0306	345145	346431	F	pdhC-Dihydrolipoamide Acetyltransferase-(CT247)
CPn0307	348986	346515	F	glgP-Glycogen Phosphorylase-(CT248)
CPn0308	349234	349596	F	similarity to CT249
CPn0309	350974	349595	R	dnaA_1-Replication Initiation Protein_1-(CT250)
CPn0310	353433	351049	R	60IM-60kDa Inner Membrane Protein-(CT251)
CPn0311	354438	353575	R	lgt-Prolipoprotein Diacylglycerol Transferase-(CT252)
CPn0312	354524	354976	F	CT101 hypothetical protein
CPn0313	354990	355355	F	acpS-Acyl-carrier Protein Synthase-(CT100)
CPn0314	356285	355353	R	trxS-Thioredoxin Reductase-(CT099)
CPn0315	356977	358716	F	rsl-S1 Ribosomal Protein-(CT098)
CPn0316	358820	360121	F	nusA-N Utilization Protein A-(CT097)
CPn0317	360081	362750	F	infB-Initiation Factor-2-(CT096)
CPn0318	362767	363126	F	rbfA-Ribosome Binding Factor A-(CT095)
CPn0319	363175	363879	F	truB-tRNA Pseudouridine Synthase-(CT094)
CPn0320	363860	364783	F	ribF-PAD Synthase-(CT093)
CPn0321	365858	364767	R	ychF-GTP Binding Protein-(CT092)
CPn0322	366249	367328	F	yscU-YopS Translocation Protein U -(CT091)
CPn0323	367331	369460	F	lcrD- Low Calcium Response D-(CT090)
CPn0324	369492	370688	F	lcrE- Low Calcium Response E-(CT089)
CPn0325	370708	371148	F	sycE-Secretion Chaperone-(CT088)
CPn0326	371148	372725	F	malQ-Glucanotransferase-(CT087)
CPn0327	372945	373211	F	rl28-L28 Ribosomal Protein-(CT086)
CPn0328	373241	374992	F	CT085 hypothetical protein
CPn0329	375088	376146	F	Phospholipase D Superfamily [leader (33) peptide]-(CT084)
CPn0330	376675	376202	R	CT083 hypothetical protein
CPn0331	378437	376701	R	CT082 hypothetical protein
CPn0332	378655	378536	R	CHLTR T2 Protein-(CT081)
CPn0333	379090	378800	R	ltuB-(CT080)
CPn0334	379311	379823	F	CT079 similarity
CPn0335	379817	380674	F	fold-Methylene Tetrahydrofolate Dehydrogenase-(CT078)
CPn0336	380650	381591	F	yojL-(CT077)
CPn0337	382027	381575	R	smpB- Small Protein B-(CT076)
CPn0338	382278	383375	F	dnaN-DNA Pol III (beta chain)-(CT075)
CPn0339	383420	384034	F	recF-ABC superfamily ATPase-(CT074)
CPn0340	383842	384156	F	(frame-shift with 0339)
CPn0341	384160	384495	F	(frame-shift with 0340)
CPn0342	384622	385062	F	predicted OMP [leader (19) peptide]-(CT073)
CPn0343	384999	385595	F	(frame-shift with 03427)
CPn0344	387420	385558	R	yaeL-Metalloprotease-(CT072)
CPn0345	388572	387436	R	yaeM-(CT071)
CPn0346	389675	388704	R	troD/ycgD-Integral Membrane Protein-(CT070)
CPn0347	391021	389678	R	troC/ycgC-Integral Membrane Protein-(CT069)
CPn0348	391803	391027	R	troB/ycgB-ABC transporter ATPase-(CT068)
CPn0349	392770	391790	R	troA/ycgA-Solute Protein Binding Family-(CT067)
CPn0350	393181	393684	F	CT066 hypothetical protein
CPn0351	393888	395432	F	adC_1-ADP/ATP Translocase_1-(CT065)

WO 00/27994

PCT/US99/26923

CPn0352	395574	396830	F	
CPn0353	396893	397135	F	
CPn0354	397167	398507	F	
CPn0355	399889	398591	R	
CPn0356	400459	400109	R	
CPn0357	401317	400469	R	
CPn0358	401751	401578	R	
CPn0359	402012	403817	F	lepA-GTPase-(CT064)
CPn0360	405358	403922	R	gnd-6-Phosphogluconate Dehydrogenase-(CT063)
CPn0361	406647	405382	R	tyrS-tyrosyl tRNA Synthetase-(CT062)
CPn0362	407825	407055	R	fliA/rpsD-Sigma-28/WhiG Family-(CT061)
CPn0363	409688	407943	R	flhA-Flagellar Secretion Protein-(CT060)
CPn0364	409966	410238	F	fer4-Ferredoxin IV-(CT059)
CPn0365	410528	411544	F	
CPn0366	411976	412440	F	
CPn0367	413102	413836	F	
CPn0368	413790	414107	F	
CPn0369	414351	415562	F	CT058 hypothetical protein_2
CPn0370	415800	416912	F	CT058 hypothetical protein_3
CPn0371	417147	417503	F	
CPn0372	417687	418001	F	
CPn0373	418380	420218	F	gcpE-(CT057)
CPn0374	420218	420961	F	CT056 hypothetical protein
CPn0375	421121	421615	F	
CPn0376	421854	422294	F	
CPn0377	423438	422347	R	sucB_1-Dihydrolipoamide Succinyltransferase_1-(CT055)
CPn0378	426168	423445	R	sucA-Oxoglutarate Dehydrogenase-(CT054)
CPn0379	426322	426765	F	CT053 hypothetical protein
CPn0380	426758	427876	F	hemW_1-Coproporphyrinogen III Oxidase_1-(CT052)
CPn0381	429809	428037	R	CT326 similarity
CPn0382	430749	430036	R	yabC/yraL-SAM-Dependent Methyltransferase-(CT048)
CPn0383	431693	430749	R	CT047 hypothetical protein
CPn0384	432377	431862	R	hctB-Histone-like Protein 2-(CT046)
CPn0385	434018	432522	R	pepA-Leucyl Aminopeptidase A-(CT045)
CPn0386	434525	434046	R	ssb-SS DNA Binding Protein-(CT044)
CPn0387	435196	434699	R	CT043 hypothetical protein
CPn0388	435329	437320	F	glgX-Glycogen Hydrolase (debranching)-(CT042)
CPn0389	438134	437319	R	CT041 hypothetical protein
CPn0390	439144	438134	R	ruvB-Holliday Junction Helicase-(CT040)
CPn0391	439692	439510	R	
CPn0392	439814	440383	F	dcd-dCTP Deaminase-(CT039)
CPn0393	440379	440723	F	CT038 hypothetical protein
CPn0394	440736	441968	F	tlyC_1-CBS Domain protein (Hemolysin Homolog)_1-(CT256)
CPn0395	441964	443175	F	CT257 hypothetical protein
CPn0396	444353	443241	R	yhfO-Nifs-related protein-(CT258)
CPn0397	445115	444381	R	PP2C phosphatase family-(CT259)
CPn0398	445533	445700	F	
CPn0399	445879	446523	F	CT253 hypothetical protein
CPn0400	446536	447306	F	CT254 hypothetical protein
CPn0401	447884	447495	R	CT255 hypothetical protein
CPn0402	448994	447888	R	mutY-Adenine Glycosylase-(CT107)
CPn0403	449015	449710	F	yceC-predicted pseudouridine synthetase family-(CT106)
CPn0404	450887	449871	R	
CPn0405	451739	450966	R	CT105 hypothetical protein
CPn0406	451969	452865	F	fabI-Enoyl-Acyl-Carrier Protein Reductase-(CT104)
CPn0407	453742	452858	R	HAD superfamily hydrolase/phosphatase-(CT103)
CPn0408	454105	454581	F	CT102 hypothetical protein
CPn0409	454645	455127	F	CT260 hypothetical protein
CPn0410	455123	455833	F	dnaQ_1-DNA Pol III Epsilon Chain_1-(CT261)
CPn0411	455833	456609	F	CT262 hypothetical protein
CPn0412	456590	457246	F	CT263 hypothetical protein
CPn0413	459203	457227	R	msbA-Transport ATP Binding Protein-(CT264)
CPn0414	460143	459172	R	accA-AcCoA Carboxylase/Transferase Alpha-(CT265)
CPn0415	461498	460221	R	CT266 hypothetical protein
CPn0416	461856	461557	R	himD/ihfA-Integration Host Factor Alpha-(CT267)
CPn0417	463035	462244	R	amiA-N-Acetylmuramoyl Alanine Amidase-(CT268)
CPn0418	464401	462953	R	murE-N-Acetylmuramoylalananylgutamy DAP Ligase-(CT269)
CPn0419	466834	464876	R	pbp3- transglycolase/transpeptidase-(CT270)
CPn0420	467108	466824	R	CT271 hypothetical protein
CPn0421	467998	467108	R	yabC-PBP2B Family methyltransferase-(CT272)
CPn0422	468242	468784	F	CT273 hypothetical protein
CPn0423	468791	469216	F	CT274 hypothetical protein



WO 00/27994

PCT/US99/26923

CPn0424	469612	470961	F	dnaA_2-Replication Initiation Factor_4-(CT275)
CPn0425	470980	471564	F	CT276 hypothetical proteins
CPn0426	472111	471536	R	CT277 similarity
CPn0427	472207	473715	F	nqr2-NADH (Ubiquinone) Dehydrogenase-(CT278)
CPn0428	473722	474681	F	nqr3-NADH (Ubiquinone) Oxidoreductase, Gamma-(CT279)
CPn0429	474681	475319	F	nqr4-NADH (Ubiquinone) Reductase 4-(CT280)
CPn0430	475326	476093	F	nqr5-NADH (Ubiquinone) Reductase 5-(CT281)
CPn0431	476483	476151	R	
CPn0432	476816	476514	R	
CPn0433	477273	476929	R	gcsH-Glycine Cleavage System H Protein-(CT282)
CPn0434	479462	477276	R	CT283 hypothetical protein
CPn0435	480902	479475	R	Phospholipase D superfamily [uncleavable leader peptide]-(CT284)
CPn0436	481618	480902	R	lpIA-Lipoate Protein Ligase-Like Protein-(CT285)
CPn0437	481816	484350	F	clpC-ClpC Protease-(CT286)
CPn0438	485416	484334	R	ycbF-PP-loop superfamily ATPase-(CT287)
CPn0439	485553	486077	F	
CPn0440	486105	486740	F	
CPn0441	486891	487838	F	CT007 hypothetical protein
CPn0442	488013	488528	F	CT006 hypothetical protein
CPn0443	488729	489979	F	CT005 hypothetical protein
CPn0444	490287	494507	F	pmp_6-Polymorphic Outer Membrane Protein G/I Family
CPn0445	494772	497579	F	pmp_7-Polymorphic Outer Membrane Protein G Family
CPn0446	497626	500415	F	pmp_8-Polymorphic Outer Membrane Protein G Family
CPn0447	500568	503351	F	pmp_9-Polymorphic Outer Membrane Protein G/I Family
CPn0448	504810	503698	R	*yxjG_Bs_2 Hypothetical Protein
CPn0449	507231	505330	R	pmp_10-PMP_10 (Frame-shift with 0451)
CPn0450	508112	507180	R	pmp_10-Polymorphic Outer Membrane Protein G Family
CPn0451	508275	511058	F	pmp_11-Polymorphic Outer Membrane Protein G Family
CPn0452	511319	512860	F	pmp_12-Polymorphic Outer Membrane Protein A/I Family (truncated)
CPn0453	513234	516152	F	pmp_13 -Polymorphic Outer Membrane Protein G Family
CPn0454	516182	519115	F	pmp_14-Polymorphic Outer Membrane Protein H Family
CPn0455	520348	519458	R	
CPn0456	521532	520327	R	
CPn0457	523865	522120	R	
CPn0458	526320	524236	R	
CPn0459	527005	526619	R	
CPn0460	527840	526992	R	
CPn0461	528638	527844	R	
CPn0462	531052	529037	R	
CPn0463	532357	531191	R	
CPn0464	532842	532366	R	
CPn0465	533212	532871	R	
CPn0466	533724	536537	F	pmp_15-Polymorphic Outer Membrane Protein E Family
CPn0467	536633	539434	F	pmp_16-Polymorphic Outer Membrane Protein E Family
CPn0468	539632	540432	F	pmp_17-Polymorphic Outer Membrane Protein E Family
CPn0469	540399	541460	F	pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with 0469)
CPn0470	541357	542532	F	pmp_17-Polymorphic Outer Membrane Protein (Frame-shift with 0470)
CPn0471	542564	545401	F	pmp_18-Polymorphic Outer Membrane Protein E/F Family
CPn0472	547905	545581	R	
CPn0473	549593	548070	R	
CPn0474	551573	549807	R	CT365 hypothetical protein
CPn0475	553844	551685	R	glgB-Glucan Branching Enzyme-(CT866)
CPn0476	554844	553858	R	CT865 hypothetical protein
CPn0477	556106	554844	R	*yqeV_Bs Hypothetical Protein
CPn0478	557625	556210	R	hflX-GTP Binding Protein-(CT379)
CPn0479	558425	557616	R	phnF-Metal Dependent Hydrolase-(CT380)
CPn0480	559303	558650	R	CT383 hypothetical protein
CPn0481	560946	559339	R	
CPn0482	561737	560961	R	artJ-Arginine Periplasmic Binding Protein-(CT381)
CPn0483	561836	564964	F	
CPn0484	564970	565824	F	aroG-Deoxyheptonate Aldolase-(CT382)
CPn0485	566038	566229	F	CT382.1 hypothetical protein
CPn0486	567784	566405	R	*hypothetical proline permease
CPn0487	569740	568112	R	CT384 hypothetical protein
CPn0488	570096	569767	R	hitA-HIT Family Hydrolase-(CT385)
CPn0489	570965	570096	R	CT386 hypothetical protein
CPn0490	571279	573333	F	CT387 hypothetical protein
CPn0491	574352	573336	R	CT389 hypothetical protein
CPn0492	574652	574804	F	
CPn0493	575004	574855	R	
CPn0494	575364	575146	R	
CPn0495	575603	576793	F	aspC-Aspartate Aminotransferase-(CT390)

WO 00/27994

PCT/US99/26923

CPn0496	576793	577812	F	CT391 hypothetical protein
CPn0497	578089	577820	R	CT388 hypothetical protein
CPn0498	579035	578085	R	
CPn0499	580359	579205	R	
CPn0500	580659	582362	F	proS-Prolyl tRNA Synthetase-(CT393)
CPn0501	582457	583650	F	hrcA-MTH Transcriptional Repressor-(CT394)
CPn0502	583650	584201	F	grpE-HSP-70 Cofactor-(CT395)
CPn0503	584234	586213	F	dnaK-HSP-70-(CT396)
CPn0504	586487	588514	F	vacB-ribonuclease family-(CT397)
CPn0505	588519	589106	F	*3-methyladenine DNA glycosylase
CPn0506	589172	589840	F	CT421 hypothetical protein
CPn0507	589961	590122	F	CT421.1 hypothetical protein
CPn0508	590142	590300	F	CT421.2 hypothetical protein
CPn0509	590335	590808	F	(predicted Metalloenzyme)-(CT422)
CPn0510	590813	591973	F	ctlyC_2-CBS Domains (Hemolysin homolog)_2-(CT423)
CPn0511	592141	592488	F	rabV_1-Sigma Regulatory Factor_1-(CT424)
CPn0512	592553	594412	F	CT425 hypothetical protein
CPn0513	594647	595753	F	Fe-S oxidoreductase_1-(CT426)
CPn0514	595729	596520	F	CT427 hypothetical protein
CPn0515	596492	597181	F	ubiE-Ubiquinone Methyltransferase-(CT428)
CPn0516	598814	597255	R	
CPn0517	599631	598795	R	
CPn0518	600803	599832	R	CT429 hypothetical protein
CPn0519	601674	600904	R	dapF-Diaminopimulate Epimerase-(CT430)
CPn0520	602218	601646	R	clpP-CLP Protease-(CT431)
CPn0521	603797	602241	R	glyA-Serine Hydroxymethyltransferase-(CT432)
CPn0522	603987	604655	F	CT433 hypothetical protein
CPn0523	604723	605052	F	
CPn0524	605103	606179	F	
CPn0525	606522	607283	F	CT398 hypothetical protein
CPn0526	608696	607710	R	yrhH-GutQ/KpsF Family Sugar-P Isomerase-(CT399)
CPn0527	609904	608726	R	sucB_2-Dihydrolipoamide Succinyltransferase_2-(CT400)
CPn0528	611162	609921	R	glcT-Glutamate Symport-(CT401)
CPn0529	612259	611165	R	ycaH-ATPase-(CT402)
CPn0530	613254	612460	R	spoU_1-rRNA Methylase_1-(CT403)
CPn0531	614069	613245	R	SAM dependent methyltransferase-(CT404)
CPn0532	614674	614075	R	ribC/risA-Riboflavin Synthase-(CT405)
CPn0533	614930	615385	F	CT406 hypothetical protein
CPn0534	615413	615784	F	dksA-DnaK Suppressor-(CT407)
CPn0535	615793	616296	F	lspA-Lipoprotein Signal Peptidase-(CT408)
CPn0536	616345	617691	F	dagA_1-D-Ala/Gly Permease_1-(CT409)
CPn0537	617833	618189	F	CT814.1 hypothetical protein
CPn0538	618212	618511	F	CT814 hypothetical protein
CPn0539	618705	621545	F	pmp_19-polymorphic outer membrane protein A Family -(CT412)
CPn0540	621694	626862	F	pmp_20-polymorphic outer membrane protein B Family-(CT413)
CPn0541	627170	628003	F	Solute binding protein (-yebL-Synechocystis Adhesin Homolog)-(CT415)
CPn0542	628003	628737	F	ABC Transporter ATPase-(CT416)
CPn0543	628725	629603	F	(Metal Transport Protein)-(CT417)
CPn0544	630529	629525	R	yhbZ-GTP binding protein-(CT418)
CPn0545	630884	630633	R	r127-L27 ribosomal protein-(CT419)
CPn0546	631229	630912	R	r121-L21 Ribosomal Protein-(CT420)
CPn0547	631661	632188	F	ygbB family-(CT434)
CPn0548	632231	632191	R	cysJ-Sulfite Reductase-(CT435)
CPn0549	633569	633255	R	rs10-S10 Ribosomal Protein-(CT436)
CPn0550	635661	633580	R	fusA-Elongation Factor G-(CT437)
CPn0551	636168	635698	R	rs7-S7 Ribosomal Protein-(CT438)
CPn0552	636587	636219	R	rs12-S12 Ribosomal Protein-(CT439)
CPn0553	637747	636812	R	
CPn0554	637854	638141	F	CT440 hypothetical protein
CPn0555	638298	640241	F	tsp-Tail-Specific Protease-(CT441)
CPn0556	640912	640325	R	crpA-15kDa Cysteine-Rich Protein-(CT442)
CPn0557	642861	641194	R	omcB-60kDa Cysteine-Rich Outer Membrane Complex Protein-(CT443)
CPn0558	643300	643031	R	omcA-9kDa-Cysteine-Rich Outer Membrane Complex Lipoprotein-(CT444)
CPn0559	643742	643927	F	CT441.1 hypothetical protein
CPn0560	645612	644098	R	glcX-Glutamyl-tRNA Synthetase-(CT445)
CPn0561	646404	645871	R	euc-CHLPS Euc Protein-(CT446)
CPn0562	648036	646918	R	*CHLPS 43 kDa protein homolog_1
CPn0563	650056	648293	R	recJ-ssDNA Exonuclease-(CT447)
CPn0564	654350	650145	R	secDsecF-Protein Export Proteins SecD/SecF (fusion)-(CT448)
CPn0565	655630	654533	R	CT449 hypothetical protein
CPn0566	656141	656890	F	yaeS family-(CT450)
CPn0567	656894	657817	F	cdaA-Phosphatidate Cytidylyltransferase-(CT451)

WO 00/27994

PCT/US99/26923

CPn0568	657817	658464	F	cdaA-Phosphatidate Cytidyltransferase-(CT452)
CPn0569	658464	659099	F	plsC-Glycerol-3-P Acyltransferase-(CT453)
CPn0570	659107	660789	F	argS-Arginyl tRNA Transferase-(CT454)
CPn0571	662122	660749	R	mraA-UDP-N-Acetylglucosamine Transferase-(CT455)
CPn0572	662352	664616	F	CT456 hypothetical protein
CPn0573	663404	664691	R	yebC family-(CT457)
CPn0574	663945	665394	R	
CPn0575	666494	665982	R	YhhY-Amino Group Acetyl Transferase-(CT458)
CPn0576	667543	666494	R	prfB-Peptide Chain Release Factor 2 (natural UGA frame-shift )-(CT459)
CPn0576	667598	667530	R	prfB-(natural UGA frame-shift )
CPn0577	667895	668155	F	SWIS (YH74) complex protein-(CT460)
CPn0578	668406	669365	F	yaeI-phosphohydrolase-(CT461)
CPn0579	669361	669993	F	ygbP/yacH-Sugar Nucleotide Phosphorylase-(CT462)
CPn0580	669993	670793	F	truA-Pseudouridylate Synthase I-(CT463)
CPn0581	671434	670745	R	Phosphoglycolate Phosphatase-(CT464)
CPn0582	671503	672177	F	CT465 hypothetical protein
CPn0583	672400	672717	F	CT466 hypothetical protein
CPn0584	672707	673798	F	atoS/ntrB-2-Component Sensor-(CT467)
CPn0585	675817	673865	F	*similarity to Cps Inca_2
CPn0586	676026	677183	F	atoC/ntrC-2-Component Regulator-(CT468)
CPn0587	677441	678124	F	*yyvD_Bs conserved hypothetical protein
CPn0588	678084	678626	F	CT469 hypothetical protein
CPn0589	678640	679395	F	CT470 hypothetical protein
CPn0590	680112	679516	F	CT471 hypothetical protein
CPn0591	680373	681020	F	yagE family-(CT472)
CPn0592	681153	681461	F	yidD family-(CT473)
CPn0593	682476	681391	F	CT474 hypothetical protein
CPn0594	682583	684958	F	pheT-phenylalanyl tRNA Synthetase Beta-(CT475)
CPn0595	684958	685926	F	CT476 hypothetical protein
CPn0596	685939	686457	F	ada-methyltransferase-(CT477)
CPn0597	688215	686479	R	oppC_2-Oligopeptide Permease_2-(CT478)
CPn0598	689697	688219	R	oppB_2-Oligopeptide Permease_2-(CT479)
CPn0599	691802	689682	R	oppA_5-oligopeptide Binding Lipoprotein_5-(CT480)
CPn0600	692147	691827	R	
CPn0601	693053	692736	R	CT483 hypothetical protein
CPn0602	694105	693104	R	CT484 hypothetical protein
CPn0603	694205	695185	F	hemZ-Ferrochetalase-(CT485)
CPn0604	695945	695196	R	flhY-Glutamine Binding Protein-(CT486)
CPn0605	696707	696150	R	yhhF-Methylase -(CT487)
CPn0606	697444	696707	R	CT488 hypothetical protein
CPn0607	698895	697573	R	glgC-Glucose-1-P Adenyltransferase-(CT489)
CPn0608	699645	699016	R	*pyrF-Uridine 5'-Monophosphate Synthase (Ump Synthase)-truncated?
CPn0609	699705	699986	F	CT490 hypothetical protein
CPn0610	701420	700029	R	rho-Transcription Termination Factor-(CT491)
CPn0611	702025	701420	R	yacE-predicted phosphatase/kinase-(CT492)
CPn0612	704631	702022	R	polA-DNA Polymerase I-(CT493)
CPn0613	705656	704658	R	sohB-Protease-(CT494)
CPn0614	707402	705783	R	adt_2-ADP/ATP Translocase_2-(CT495)
CPn0615	708137	707634	R	pgsA_1-Glycerol-3-P Phosphatidyltransferase_1-(CT496)
CPn0616	708791	710137	F	dnaB-Replicative DNA Helicase-(CT497)
CPn0617	710484	712316	F	gldA-FAD-dependent oxidoreductase-(CT498)
CPn0618	712306	713010	F	lplA-Lipoate-Protein Ligase A-(CT499)
CPn0619	713444	713013	R	ndk-Nucleoside-2-P Kinase-(CT500)
CPn0620	714139	713519	R	ruvA-Holliday Junction Helicase-(CT501)
CPn0621	714647	714144	R	ruvC-Crossover Junction Endonuclease-(CT502)
CPn0622	715752	714793	R	CT503 hypothetical protein
CPn0623	716993	716163	R	CT504 hypothetical protein
CPn0624	718015	717011	R	gapA-Glyceraldehyde-3-P Dehydrogenase-(CT505)
CPn0625	718485	718060	R	r117-L17 Ribosomal Protein-(CT506)
CPn0626	719616	718495	R	rpoA-RNA Polymerase Alpha-(CT507)
CPn0627	720038	719640	R	rsl1-S11 Ribosomal Protein-(CT508)
CPn0628	720428	720063	R	rsl3-S13 Ribosomal Protein-(CT509)
CPn0629	721857	720487	R	secY-Translocase-(CT510)
CPn0630	722316	721885	R	r115-L15 Ribosomal Protein-(CT511)
CPn0631	722806	722312	R	rs5-S5 Ribosomal Protein-(CT512)
CPn0632	723195	722827	R	r118-L18 Ribosomal Protein-(CT513)
CPn0633	723757	723209	R	r16-L6 Ribosomal Protein-(CT514)
CPn0634	724185	723787	R	rs8-S8 Ribosomal Protein-(CT515)
CPn0635	724745	724206	R	r15-L5 Ribosomal Protein-(CT516)
CPn0636	725082	724750	R	r124-L24 Ribosomal Protein-(CT517)
CPn0637	725464	725099	R	r114-L14 Ribosomal Protein-(CT518)
CPn0638	725747	725490	R	rsl7-S17 Ribosomal Protein-(CT519)

WO 00/27994

PCT/US99/26923

CPn0639	725958	725743	R	r129-L29 Ribosomal Protein-(CT520)
CPn0640	726377	725964	R	r116-L16 Ribosomal Protein-(CT521)
CPn0641	727077	726409	R	rs3-S3 Ribosomal Protein-(CT522)
CPn0642	727428	727096	R	r122-L22 Ribosomal Protein-(CT523)
CPn0643	727713	727450	R	rs19-S19 Ribosomal Protein-(CT524)
CPn0644	728573	727722	R	r12-L2 Ribosomal Protein-(CT525)
CPn0645	728930	728598	R	r123-L23 Ribosomal Protein-(CT526)
CPn0646	729621	728950	R	r14-L4 Ribosomal Protein-(CT527)
CPn0647	730331	729657	R	r13-L3 Ribosomal Protein-(CT528)
CPn0648	731603	730605	R	CT529 hypothetical protein
CPn0649	732672	731710	R	fmc-Methionyl tRNA Formyltransferase-(CT530)
CPn0650	733501	732665	R	lpxA-Acyl-Carrier UDP-GlcNAc -(CT531)
CPn0651	733975	733517	R	fabZ-Myristoyl-Acyl Carrier Dehydratase-(CT532)
CPn0652	734835	733990	R	lpxC-Myristoyl GlcNAc Deacetylase-(CT533)
CPn0653	736490	734868	R	cutE-Apolipoprotein N-Acetyltransferase-(CT534)
CPn0654	736967	736503	R	vd1D/yc1A-acyl-CoA Thioesterase-(CT535)
CPn0655	737847	737101	R	dnaQ_2-DNA Pol III Epsilon Chain_2-(CT536)
CPn0656	737872	738048	F	
CPn0657	738473	738051	R	yjeE (ATPase or Kinase)-(CT537)
CPn0658	739168	738455	R	CT538 hypothetical protein
CPn0659	739533	739838	F	trxA-Thioredoxin-(CT539)
CPn0660	740327	739860	R	spoU_2-rRNA Methylase_2-(CT540)
CPn0661	741100	740327	R	mip-FKBP-type peptidyl-prolyl cis-trans isomerase-(CT541)
CPn0662	742923	741172	R	aspS-Aspartyl tRNA Synthetase-(CT542)
CPn0663	744190	742901	R	hisS-Histidyl tRNA Synthetase-(CT543)
CPn0664	744757	744557	R	
CPn0665	745001	746365	F	uhpC-Hexosphosphate Transport -(CT544)
CPn0666	746388	750107	F	dnaE-DNA Pol III Alpha-(CT545)
CPn0667	751058	750177	R	predicted OMP (leader 17)-(CT546)
CPn0668	751209	752162	F	CT547 hypothetical protein
CPn0669	752179	752775	F	CT548 hypothetical protein
CPn0670	752765	753196	F	rsbW-sigma regulatory factor-histidine kinase-(CT549)
CPn0671	753630	753205	R	CT550 hypothetical protein
CPn0672	753741	755048	F	dacF(pbp5)-D-Ala-D-Ala Carboxypeptidase-(CT551)
CPn0673	755287	755463	F	CT552 hypothetical protein
CPn0674	756668	755577	R	fmu-RNA Methyltransferase-(CT553)
CPn0675	757919	756768	R	CT696 hypothetical protein
CPn0676	759217	758051	R	homologous to CT695
CPn0677	760401	759256	R	
CPn0678	761320	760682	R	
CPn0679	762930	761725	R	pgk-Phosphoglycerate Kinase-(CT693)
CPn0680	764248	762971	R	ygo4-Phosphate Permease-(CT692)
CPn0681	764929	764258	R	CT691 hypothetical protein
CPn0682	764984	765955	F	dppD-ABC ATPase Dipeptide Transport-(CT690)
CPn0683	765948	766919	F	dppF-ABC ATPase Dipeptide Transport-(CT689)
CPn0684	768038	767181	R	spoJ/parB-Chromosome Partitioning Protein-(CT688)
CPn0685	768068	768217	F	
CPn0686	768361	768176	R	
CPn0687	768564	769214	F	CT482 hypothetical protein
CPn0688	769382	770137	F	CT481 hypothetical protein
CPn0689	771404	770187	R	yfhO_1-NifS-related Aminotransferase_1-(CT687)
CPn0690	772680	771436	R	ABC Transporter Membrane Protein-(CT686)
CPn0691	773452	772685	R	abcX-ABC Transporter ATPase-(CT685)
CPn0692	774912	773461	R	ABC Transporter-(CT684)
CPn0693	776256	775240	R	TPR Repeats (O-Linked GlcNAc Transferase similarity)-(CT683)
CPn0694	779599	776330	R	pbp2-PBP2-transglycolase/transpeptidase-(CT682)
CPn0695	780216	781382	F	ompA-Major Outer Membrane Protein-(CT681)
CPn0696	781769	782599	F	rs2-S2 Ribosomal Protein-(CT680)
CPn0697	782602	783447	F	tsf-Elongation Factor TS-(CT679)
CPn0698	783458	784201	F	pyrH-UMP Kinase-(CT679)
CPn0699	784182	784721	F	rrf-Ribosome Releasing Factor-(CT677)
CPn0700	785097	785609	F	CT676 hypothetical protein
CPn0701	785599	786672	F	karG-Arginine Kinase-(CT675)
CPn0702	789685	789629	R	yscC/gspD-Yop C/Gen Secretion Protein D-(CT674)
CPn0703	791190	789685	R	pkn5-S/T Protein Kinase-(CT673)
CPn0704	792321	791209	R	filN- Flagellar Motor Switch Domain/YscQ family-(CT672)
CPn0705	793173	792334	R	CT671 hypothetical protein
CPn0706	793683	793180	R	CT670 hypothetical protein
CPn0707	795029	793704	R	yscN-Yop N (Flagellar-Type ATPase)-(CT669)
CPn0708	795705	795034	R	CT668 hypothetical protein
CPn0709	796188	795742	R	CT667 hypothetical protein
CPn0710	796461	796210	R	CT666 hypothetical protein

WO 00/27994

PCT/US99/26923

CPn0711	796731	796486	R	CT665 hypothetical protein
CPn0712	799315	796781	R	FHA domain; homology to adenylate cyclase)-(CT664)
CPn0713	799721	799332	R	CT663 hypothetical protein
CPn0714	801107	800091	R	hema-Glutamyl tRNA Reductase-(CT662)
CPn0715	801657	803462	F	gyrB_2-DNA Gyrase Subunit B_2-(CT661)
CPn0716	803469	804902	F	gyrA_2-DNA Gyrase Subunit A_2-(CT660)
CPn0717	805010	805306	F	CT656 hypothetical protein
CPn0718	805309	805626	F	CT657 hypothetical protein
CPn0719	805916	806890	F	sfhB-(Pseudouridine Synthase)-(CT658)
CPn0720	807003	807236	F	CT659 hypothetical protein
CPn0721	807683	808489	F	kdsA-KDO Synthetase-(CT655)
CPn0722	808489	808974	F	CT654 hypothetical protein
CPn0723	808984	809703	F	yhbG-ABC Transporter ATPase-(CT653)
CPn0724	810527	809706	R	
CPn0725	810811	810587	R	CT652.1 hypothetical protein
CPn0726	813372	810880	R	CT620 hypothetical protein
CPn0727	813577	816192	F	CT619 hypothetical protein
CPn0728	818477	816525	R	CHLPN 76kDa Homolog_1 (CT622)
CPn0729	819857	818592	R	CHLPN 76kDa Homolog_2 (CT623)
CPn0730	821603	819963	R	mviN-Integral Membrane Protein-(CT624)
CPn0731	821587	821760	F	
CPn0732	822098	822976	F	nfo-Endonuclease IV-(CT625)
CPn0733	823727	823101	R	rs4-S4 Ribosomal Protein-(CT626)
CPn0734	823944	824915	F	yceA-(CT627)
CPn0735	825668	825003	R	*pyrH/udk-Uridine Kinase (Uridine Monophosphokinase) (Pyrimidine Ribonucleoside Kinase).
CPn0736	827686	825992	R	ygeD-Efflux Protein-(CT641)
CPn0737	827685	830756	F	recC-Exodeoxyribonuclease V, Gamma-(CT640)
CPn0738	830746	833895	F	recB-Exodeoxyribonuclease V, Beta-(CT639)
CPn0739	834871	833861	R	CT638 hypothetical protein
CPn0740	836048	834864	R	tyrB-Aromatic AA Amino transferase-(CT637)
CPn0741	838350	836185	R	greA-Transcription Elongation Factor-(CT636)
CPn0742	838463	838888	F	CT635 hypothetical protein
CPn0743	838962	840362	F	nqrA-Ubiquinone Oxidoreductase, Alpha-(CT634)
CPn0744	841384	840389	R	hemB-Porphobilinogen Synthase-(CT633)
CPn0745	841903	841742	R	
CPn0746	841975	843567	F	CT632 hypothetical protein
CPn0747	843675	843740	F	CT631 hypothetical protein
CPn0747	843725	843910	F	CT631 hypothetical protein (frame-shift)
CPn0748	844987	844121	R	ispa-Geranyl Transtransferase-(CT628)
CPn0749	845629	845006	R	glmU-UDP-GlcNAc Pyrophosphorylase-(CT629)
CPn0750	846411	845707	R	tctD/cpxR-HTX Transcriptional Regulatory Protein + Receiver Domain-(CT630)
CPn0751	846608	848434	F	CT651 hypothetical protein
CPn0752	848604	850082	F	recD_2-Exodeoxyribonuclease V, Alpha_2-(CT652)
CPn0753	851006	850161	R	
CPn0754	851336	851040	R	rs20-S20 Ribosomal Protein-(CT617)
CPn0755	851597	852799	F	CT616 hypothetical protein
CPn0756	852961	854676	F	rpoD-RNA Polymerase Sigma-66 -(CT615)
CPn0757	854733	855134	F	folX-Dihydroneopterin Aldolase-(CT614)
CPn0758	855110	856459	F	folP/dhps-Dihydropteroate Synthase-(CT613)
CPn0759	856488	856997	F	folA-Dihydrofolate Reductase-(CT612)
CPn0760	856957	857694	F	CT611 hypothetical protein
CPn0761	857704	858375	F	CT610 hypothetical protein
CPn0762	859597	858539	R	recA-RecA recombination protein-(CT650)
CPn0763	860511	859972	R	ygfA-Formyltetrahydrofolate Cycloligase-(CT649)
CPn0764	861807	860524	R	CT648 hypothetical protein
CPn0765	862382	861801	R	CT647 hypothetical protein
CPn0766	863782	862394	R	CT646 hypothetical protein
CPn0767	863884	864177	F	CT645 hypothetical protein
CPn0768	864159	865163	F	yohI/nirJ-predicted oxidoreductase -(CT644)
CPn0769	867733	865121	R	topA-DNA Topoisomerase I-Fused to SWI Domain-(CT643)
CPn0770	868340	869131	F	CT642 hypothetical protein
CPn0771	870463	869144	R	rpoN-RNA Polymerase Sigma-54-(CT609)
CPn0772	872385	870469	R	uvrD-DNA Helicase-(CT608)
CPn0773	872488	873195	F	ung-Uracil DNA Glycosylase-(CT607)
CPn0774	873195	873425	F	CT606.1 hypothetical protein
CPn0775	874031	873414	R	yggV family-(CT606)
CPn0776	874246	875487	F	CT605 hypothetical protein
CPn0777	875601	877178	F	groEL_2-heat shock protein-60 -(CT604)
CPn0778	877505	878092	F	tsa/ahpC-Thio-specific Antioxidant (TSA) Peroxidase-(CT603)
CPn0779	878481	878095	R	CT602 hypothetical protein

WO 00/27994

PCT/US99/26923

CPn0780	879205	878591	R	papQ/amiB-N-Acetylmuramoyl-L-Ala Amidase-(CT601)
CPn0781	879773	879198	R	pal-Peptidoglycan-Associated Lipoprotein-(CT600)
CPn0782	881065	879773	R	tolB-polysaccharide transporter-(CT599)
CPn0783	881885	881100	R	CT598 hypothetical protein
CPn0784	882296	881892	R	exbD-Biopolymer Transport Protein-(CT597)
CPn0785	882991	882296	R	exbB/tolQ-polysaccharide transporter-(CT596)
CPn0786	883185	885293	F	dsbD/xprA-Thio:disulfide Interchange Protein-(CT595)
CPn0787	885619	886401	F	yabD/yciH-PHP superfamily (urease/pyrimidinase) hydrolase-(CT594)
CPn0788	886542	887432	F	sdhC-Succinate Dehydrogenase-(CT593)
CPn0789	887439	889316	F	sdhA-Succinate Dehydrogenase-(CT592)
CPn0790	889330	890103	F	sdhB-Succinate Dehydrogenase-(CT591)
CPn0791	893050	890111	R	CT590 hypothetical protein
CPn0792	894919	893108	R	CT589 hypothetical protein
CPn0793	896823	894919	R	rbsU-sigma regulatory family protein-PP2C phosphatase (RsbW antagonist)-(CT588)
CPn0794	897174	898004	F	
CPn0795	898128	899195	F	
CPn0796	899301	901340	F	
CPn0797	901600	902694	F	
CPn0798	902846	903856	F	
CPn0799	904986	903940	R	
CPn0800	906532	905249	R	eno-Enolase-(CT587)
CPn0801	908697	906727	R	uvrB-Exinuclease ABC Subunit B-(CT586)
CPn0802	909740	908709	R	trpS-Tryptophanyl tRNA Synthetase-(CT585)
CPn0803	910303	909752	R	CT584 hypothetical protein
CPn0804	911059	910310	R	gp6D-CHLTR Plasmid Paralog-(CT583)
CPn0805	911831	911067	R	minD-chromosome partitioning ATPase-CHLTR plasmid protein GP5D-(CT582)
CPn0806	913771	911867	R	thrS-Threonyl tRNA Synthetase-(CT581)
CPn0807	913971	914879	F	CT580 hypothetical protein
CPn0808	916287	914956	R	CT579 hypothetical protein
CPn0809	917785	916307	R	CT578 hypothetical protein
CPn0810	918184	917825	R	CT577 hypothetical protein
CPn0811	918900	918208	R	lcrK_1-Low Ca Response Protein K_1-(CT576)
CPn0812	919123	920862	F	mutL-DNA Mismatch Repair-(CT575)
CPn0813	920870	921934	F	pepP-Aminopeptidase P-(CT574)
CPn0814	922107	923357	F	CT573 hypothetical protein
CPn0815	923361	925622	F	gspD/pilQ-Gen. Secretion Protein D-(CT572)
CPn0816	925615	927102	F	gspE-Gen. Secretion Protein E-(CT571)
CPn0817	927115	928287	F	gspF-Gen. Secretion Protein F-(CT570)
CPn0818	928314	928682	F	predicted CMP [leader (16) peptide]-(CT569)
CPn0819	928689	929132	F	CT568 hypothetical protein
CPn0820	929120	929659	F	CT567 hypothetical protein
CPn0821	929667	930668	F	CT566 hypothetical protein
CPn0822	930756	931229	F	CT565 hypothetical protein
CPn0823	932367	931501	R	yscT/spaR-YopT Translocation T-(CT564)
CPn0824	932662	932378	R	yscS/fliQ-YopS/fliQ Translocation Protein-(CT563)
CPn0825	933594	932677	R	yscR-Yop Translocation R-(CT562)
CPn0826	934310	933612	R	yscL-Yop Translocation L-(CT561)
CPn0827	935264	934434	R	CT560 hypothetical protein
CPn0828	936271	935267	R	yscJ-Yop Translocation J-(CT559)
CPn0829	936744	937298	F	
CPn0830	937444	937959	F	
CPn0831	938267	938434	F	
CPn0832	939747	938827	R	lipA-Lipoate Synthetase-(CT558)
CPn0833	941129	939747	R	lpdA-Lipoamide Dehydrogenase-(CT557)
CPn0834	941553	942014	F	CT556 hypothetical protein
CPn0835	945689	942045	R	mot1_1-SWI/SNF family helicase_1-(CT555)
CPn0836	946879	945722	R	brnQ-Amino Acid (Branched) Transport-(CT554)
CPn0837	947771	947145	R	nth-Endonuclease III-(CT697)
CPn0838	949106	947781	R	thdF-Thiophene/Furan Oxidation Protein-(CT698)
CPn0839	949257	950159	F	psdB-Phosphatidylserine Decarboxylase-(CT699)
CPn0840	950222	951544	F	CT700 hypothetical protein
CPn0841	951731	954640	F	secA_2-Translocase SecA_2-(CT701)
CPn0842	954883	954710	R	CT702 hypothetical protein (frame-shift with 0843)
CPn0843	955191	954994	R	CT702 hypothetical protein
CPn0844	956730	955270	R	yphC-GTPase/GTP-binding protein-(CT703)
CPn0845	958079	956650	R	pcnB_1-Poly A Polymerase_1-(CT704)
CPn0846	959374	958112	R	clpX-CLP Protease ATPase-(CT705)
CPn0847	959995	959387	R	clpP-CLP Protease Subunit-(CT706)
CPn0848	961502	960177	R	tig/murI-Trigger Factor-peptidyl-prolyl isomerase-(CT707)
CPn0849	961788	965285	F	mot1_2-SWI/SNF family helicase_2-(CT708)
CPn0850	965293	966390	F	mreB-Rod Shape Protein-Sugar Kinase-(CT709)

WO 00/27994

PCT/US99/26923

CPn0851	966396	968195	F	pckA-Phosphoenolpyruvate Carboxykinase-(CT710)
CPn0852	968316	970613	F	CT711 hypothetical protein
CPn0853	970637	971803	F	CT712 hypothetical protein
CPn0854	972837	971806	R	ompB-Outer Membrane Protein B-(CT713)
CPn0855	973995	972994	R	gpdA-Glycerol-3-P Dehydrogenase-(CT714)
CPn0856	975377	973995	R	AgX-1 Homolog-UDP-Glucose Pyrophosphorylase-(CT715)
CPn0857	975757	975392	R	CT716 hypothetical protein
CPn0858	977055	975757	R	fliI-Flagellum-specific ATP Synthase-(CT717)
CPn0859	977588	977055	R	CT718 hypothetical protein
CPn0860	978630	977608	R	fliP-Flagellar M-Ring Protein-(CT719)
CPn0861	979722	978925	R	nifU-NifU-related protein-(CT720)
CPn0862	980873	979722	R	yzhO <sub>2</sub> -NifS-related protein <sub>2</sub> -(CT721)
CPn0863	981514	980831	R	pgmA-Phosphoglycerate Mutase-(CT722)
CPn0864	981670	982374	F	yjbc-predicted pseudouridine synthase-(CT723)
CPn0865	982418	982942	F	CT724 hypothetical protein
CPn0866	983491	982916	R	birA-Biotin Synthetase-(CT725)
CPn0867	983423	984667	F	rodA-Rod Shape Protein-(CT726)
CPn0868	986643	984670	F	zntA/cadA-Metal Transport P-type ATPase-(CT727)
CPn0869	987401	986658	F	CT728 hypothetical protein
CPn0870	988728	987448	F	serS-Seryl tRNA Synthetase <sub>2</sub> -(CT729)
CPn0871	988772	989899	F	ribD-Riboflavin Deaminase-(CT730)
CPn0872	989963	991216	F	ribA&ribB-GTP Cyclohydrotase & DHBP Synthase -(CT731)
CPn0873	991233	991694	F	ribE-Ribityllumazine Synthase-(CT732)
CPn0874	993107	991749	F	CT733 hypothetical protein
CPn0875	993372	994022	F	CT734 hypothetical protein
CPn0876	994144	995517	F	dagA <sub>2</sub> -D-Alanine/Glycine Permease <sub>2</sub> -(CT735)
CPn0877	995533	995982	F	ybcL family-(CT736)
CPn0878	996654	995992	F	SET Domain protein-(CT737)
CPn0879	997439	996645	R	yycJ-metal dependent hydrolase-(CT738)
CPn0880	999861	997444	R	ftsK-Cell Division Protein FtsK-(CT739)
CPn0881	1005667	1006209	F	
CPn0882	1006268	1007404	F	
CPn0883	1008865	1007573	R	dmpP/nqr6-Phenolhydrolase/NADH ubiquinone oxidoreductase-(CT740)
CPn0884	1009359	1009009	R	CT741 hypothetical protein
CPn0885	1010635	1009433	R	ygcA-rRNA Methyltransferase-(CT742)
CPn0886	1011276	1010908	R	hctA-Histone-Like Developmental Protein-(CT743)
CPn0887	1011692	1014157	F	CHLTR possible phosphoprotein-(CT744)
CPn0888	1015423	1014119	R	hemG-protoporphyrinogen Oxidase-(CT745)
CPn0889	1016835	1015462	R	hemN <sub>2</sub> -Coproporphyrinogen III Oxidase <sub>2</sub> -(CT746)
CPn0890	1017805	1016819	R	hemE-Uroporphyrinogen Decarboxylase-(CT747)
CPn0891	1021073	1017819	R	mfd-Transcription-Repair Coupling-(CT748)
CPn0892	1023661	1021046	R	alaS-Alanyl tRNA Synthetase-(CT749)
CPn0893	1023894	1025888	F	tktB-Transketolase-(CT750)
CPn0894	1026766	1025888	R	amm-AMP Nucleosidase-(CT751)
CPn0895	1026988	1027557	F	efp <sub>2</sub> -Elongation Factor P <sub>2</sub> -(CT752)
CPn0896	1027595	1027822	F	CT753 hypothetical protein
CPn0897	1028737	1027853	R	(possible phosphohydrolase)-(CT754)
CPn0898	1030460	1028904	R	Mitochondrial HSP60 Chaperonin Homolog-(CT755)
CPn0899	1030875	1032215	F	murF-Muramoyl-DAP Ligase-(CT756)
CPn0900	1032235	1033281	F	mraY-Muramoyl-Pentapeptide Transferase-(CT757)
CPn0901	1033287	1034537	F	murD-Muramoylalanine-Glutamate Ligase-(CT758)
CPn0902	1034543	1035241	F	nlpD-Muramidase (invasin repeat family)-(CT759)
CPn0903	1035263	1036417	F	ftsW-Cell Division Protein FtsW-(CT760)
CPn0904	1036326	1037396	F	murG-Peptidoglycan Transferase-(CT761)
CPn0905	1037409	1039835	F	murC&ddlA-Muramate-Ala Ligase & D-Ala-D-Alam Ligase-(CT762)
CPn0906	1040340	1039915	R	CT763 hypothetical protein
CPn0907	1040780	1040445	R	*cutA Periplasmic Divalent Cation Tolerance Protein CutA (C-Type Cytochrome Biogenesis Protein)
CPn0908	1041589	1040780	R	CT764 hypothetical protein
CPn0909	1041637	1041966	F	rsbV <sub>2</sub> -Sigma Factor Regulator <sub>2</sub> -(CT765)
CPn0910	1041979	1043004	F	miaA-tRNA Pyrophosphate Transferase-(CT766)
CPn0911	1044043	1042985	R	Fe-S cluster oxidoreductase <sub>2</sub> -(CT767)
CPn0912	1044129	1045760	F	CT768 hypothetical protein
CPn0913	1045760	1045945	F	
CPn0914	1045999	1046397	F	
CPn0915	1046461	1046817	F	ybeB-iojap superfamily ortholog-(CT769)
CPn0916	1046837	1048084	F	fabF-Acyl Carrier Protein Synthase-(CT770)
CPn0917	1048090	1048539	F	hydrolase/phosphatase homolog-(CT771)
CPn0918	1049223	1048579	R	ppa-Inorganic Pyrophosphatase-(CT772)
CPn0919	1049378	1050430	F	ldh-Leucine Dehydrogenase-(CT773)
CPn0920	1051405	1050431	R	cysQ-Sulfite Synthesis/biphosphate phosphatase-(CT774)
CPn0921	1051535	1052293	F	snGlycerol-3-P Acyltransferase-(CT775)

WO 00/27994

PCT/US99/26923

CPn0922	1052314	1053927	F	aas-Acylglycerophosphoethanolamine Acyltransferase-(CT776)
CPn0923	1053984	1055093	F	bioF_1-Oxononanoate Synthase_1-(CT777)
CPn0924	1057274	1055028	R	priA-Primosomal Protein N'-(CT778)
CPn0925	1057900	1057226	R	CT779 hypothetical protein
CPn0926	1058060	1058557	F	Thioredoxin Disulfide Isomerase-(CT780)
CPn0927	1059809	1058670	R	*CHLPS 43 kDa protein homolog_2
CPn0928	1061008	1059884	R	*CHLPS 43 kDa protein homolog_3
CPn0929	1062292	1061186	R	*CHLPS 43 kDa protein homolog_4
CPn0930	1062857	1063330	F	
CPn0931	1064138	1065718	F	lysS-Lysyl tRNA Synthetase-(CT781)
CPn0932	1067142	1065721	R	cysS-Cysteinyl tRNA Synthetase-(CT782)
CPn0933	1067535	1068578	F	predicted disulfide bond isomerase-(CT783)
CPn0934	1068942	1068526	R	rnpA-Ribonuclease P Protein Component-(CT784)
CPn0935	1069091	1068957	R	rl34-L34 Ribosomal Protein-(CT785)
CPn0936	1069336	1069470	F	rl36-L36 Ribosomal Protein-(CT786)
CPn0937	1069496	1069798	F	rs14-S14 Ribosomal Protein-(CT787)
CPn0938	1070322	1069849	R	CT788 hypothetical protein-[leader (60) peptide-periplasmic]
CPn0939	1070728	1071195	F	CT790 hypothetical protein
CPn0940	1073012	1071204	R	uvrC-Excinuclease ABC, Subunit C-(CT791)
CPn0941	1075501	1073018	R	mutS-DNA Mismatch Repair-(CT792)
CPn0942	1075985	1077754	F	dnaG/prim-DNA Primase-(CT794)
CPn0943	1077978	1078238	F	CT794.1 hypothetical protein
CPn0944	1078512	1078997	F	
CPn0945	1079070	1079660	F	CT795 hypothetical protein
CPn0946	1082786	1079745	R	glyQ-Glycyl tRNA Synthetase-(CT796)
CPn0947	1083442	1084059	F	pgsA_2-Glycerol-3-P-Phosphatidyltransferase_2-(CT797)
CPn0948	1085474	1084047	R	glgA-Glycogen Synthase-(CT798)
CPn0949	1085929	1086483	F	ctc-General Stress Protein-(CT799)
CPn0950	1086488	1087027	F	pth-Peptidyl tRNA Hydrolase-(CT800)
CPn0951	1087122	1087457	F	rs6-S6 Ribosomal Protein-(CT801)
CPn0952	1087478	1087723	F	rs18-S18 Ribosomal Protein-(CT802)
CPn0953	1087742	1088248	F	rl9-L9 Ribosomal Protein-(CT803)
CPn0954	1088286	1088708	F	ychB-Predicted Kinase-(CT804)
CPn0955	1088612	1089175	F	(frame-shift with 0954)
CPn0956	1089560	1090909	F	CT805 hypothetical protein
CPn0957	1093788	1090963	R	ide/ptr-Insulinase family/Protease III-(CT806)
CPn0958	1094785	1093793	R	plsB-Glycerol-3-P Acyltransferase-(CT807)
CPn0959	1096343	1094799	R	cafE-Axial Filament Protein-(CT808)
CPn0960	1096764	1097102	F	CT809 hypothetical protein
CPn0961	1097118	1097297	F	rl32-L32 Ribosomal Protein-(CT810)
CPn0962	1097316	1098275	F	plsX-FA/Phospholipid Synthesis Protein-(CT811)
CPn0963	1098398	1103224	F	pmp_21-Polymorphic Outer Membrane Protein D Family-(CT812)
CPn0964	1104758	1103301	R	
CPn0965	1106736	1104925	R	lpxB-Lipid A Disaccharide Synthase-(CT411)
CPn0966	1108037	1106748	R	pcnB_2-PolyA Polymerase_2-(CT410)
CPn0967	1108512	1109885	F	mraA/pgm-Phosphoglucomutase-(CT815)
CPn0968	1109895	1111721	F	glmS-Glucosamine-Fructose-6-P Aminotransferase-(CT816)
CPn0969	1111812	1112999	F	0969-tyrP_1-Tyrosine Transport_1-(CT817) tyrP_1-Tyrosine Transport_1-(CT817)
CPn0970	1113461	1114648	F	0970-tyrP_2-Tyrosine Transport_2-(CT818) tyrP_2-Tyrosine Transport_2-(CT818)
CPn0971	1114702	1115415	F	ycca-Transport Permease-(CT819)
CPn0972	1116299	1115430	R	ftsY-Cell Division Protein FtsY-(CT820)
CPn0973	1116370	1117527	F	sucC-Succinyl-CoA Synthetase, Beta-(CT821)
CPn0974	1117544	1118422	F	sucD-Succinyl-CoA Synthetase, Alpha-(CT822)
CPn0975	1119104	1119637	F	
CPn0976	1120082	1121185	F	
CPn0977	1121371	1122402	F	
CPn0978	1122665	1123693	F	
CPn0979	1123980	1125443	F	htra-DO Serine Protease-(CT823)
CPn0980	1126982	1125504	R	*similarity to Saccharomyces cerevisiae hypothetical 52.9KD protein
CPn0981	1127031	1129952	F	Zinc Metalloprotease (insulinase family)-(CT824)
CPn0982	1131194	1129962	R	yigN family-(CT825)
CPn0983	1132000	1131206	R	pssA-Glycerol-Serine Phosphatidyltransferase-(CT826)
CPn0984	1132379	1135510	F	nrda-Ribonucleoside Reductase, Large Chain-(CT827)
CPn0985	1135534	1136571	F	nrdb-Ribonucleoside Reductase, Small Chain-(CT828)
CPn0986	1136724	1137395	F	yggH-predicted rRNA Methylase-(CT829)
CPn0987	1137516	1138115	F	ytgB-like predicted rRNA methylase-(CT830)
CPn0988	1138986	1138075	R	murB-UDP-N-Acetylenolpyruvoylglucosamine Reductase-(CT831)
CPn0989	1139495	1139016	R	CT832 hypothetical protein
CPn0990	1139883	1140440	F	infC-Initiation Factor 3-(CT833)
CPn0991	1140421	1140612	F	rl35-L35 Ribosomal Protein-(CT834)



WO 00/27994

PCT/US99/26923

CPn0992	1140634	1140996	F	r120-L20 Ribosomal Protein-(CT835)
CPn0993	1141014	1142030	F	pheS-Phenylalanyl tRNA Synthetase, Alpha-(CT836)
CPn0994	1142398	1144440	F	CT837 hypothetical protein
CPn0995	1145512	1144415	R	CT838 hypothetical protein
CPn0996	1146589	1145519	R	CT839 hypothetical protein
CPn0997	1146708	1147664	F	mesJ-PP-loop superfamily ATPase-(CT840)
CPn0998	1147855	1150584	F	ftsH-ATP-dependent zinc protease-(CT841)
CPn0999	1152847	1150766	R	pnp-Polyribonucleotide Nucleotidyltransferase-(CT842)
CPn1000	1153157	1152891	R	rel5-S15 Ribosomal Protein-(CT843)
CPn1001	1153405	1153869	F	yfhC-cytosine deaminase-(CT844)
CPn1002	1153862	1154089	F	CT845 hypothetical protein
CPn1003	1154796	1154092	R	CT846 hypothetical protein
CPn1004	1155397	1154879	R	CT847 hypothetical protein
CPn1005	1155933	1155415	R	CT848 hypothetical protein
CPn1006	1156472	1155990	R	CT849 hypothetical protein
CPn1007	1156689	1156907	F	CT849.1 hypothetical protein
CPn1008	1156928	1158223	F	CT850 hypothetical protein
CPn1009	1159058	1158186	R	map-Methionine Aminopeptidase-(CT851)
CPn1010	1159672	1159067	R	CT852 hypothetical protein
CPn1011	1160306	1159902	R	CT853 hypothetical protein
CPn1012	1162193	1160421	R	yezB-ABC transporter permease-(CT854)
CPn1013	1162245	1163624	F	fumC-Fumarate Hydratase-(CT855)
CPn1014	1165426	1163732	R	ychM-Sulfate Transporter-(CT856)
CPn1015	1165634	1166893	F	CT857 hypothetical protein (possible IM protein)
CPn1016	1167042	1168898	F	CT858 hypothetical protein
CPn1017	1169006	1169935	F	lycB-Metalloprotease-(CT859)
CPn1018	1169898	1170629	F	
CPn1019	1172128	1170638	R	CT860 hypothetical protein
CPn1020	1173679	1172150	R	CT861 hypothetical protein
CPn1021	1174213	1173698	R	lcrH_2-Low Calcium Response_2-(CT862)
CPn1022	1175673	1174216	R	CT863 hypothetical protein
CPn1023	1176035	1176331	F	
CPn1024	1177236	1176334	R	xerD-Integrase/recombinase-(CT864)
CPn1025	1177302	1178879	F	pgi-Glucose-6-P Isomerase-(CT378)
CPn1026	1178997	1179137	F	ltuA-(CT377)
CPn1027	1179175	1180755	F	
CPn1028	1181016	1181999	F	mdhC-Malate Dehydrogenase-(CT376)
CPn1029	1182008	1182844	F	
CPn1030	1183886	1182843	R	predicted D-amino acid dehydrogenase-(CT375)
CPn1031	1185552	1184098	R	arcD-Arginine/Ornithine Antiporter-(CT374)
CPn1032	1186150	1185566	R	CT373 hypothetical protein
CPn1033	1187500	1186187	R	CT372 hypothetical protein
CPn1034	1188517	1187732	R	Predicted OMP_1 (CT371) [leader (18) peptide]
CPn1035	1190000	1188570	R	AroE-Shikimate 5-Dehydrogenase-(CT370)
CPn1036	1191135	1189984	R	AroB-Dehydroquinase Synthase-(CT369)
CPn1037	1192199	1191123	R	AroC-Chorismate Synthase-(CT368)
CPn1038	1192726	1192199	R	aroL-Shikimate Kinase II-(CT367)
CPn1039	1193999	1192665	R	aroA-Phosphoshikimate Vinyltransferase-(CT366)
CPn1040	1194741	1194073	R	
CPn1041	1195994	1194726	R	*bioA-Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
CPn1042	1196590	1195934	R	*bioD-dethiobiotin synthetase
CPn1043	1197717	1196572	R	*bioF_2-Oxononanoate Synthase_2
CPn1044	1198691	1197699	R	*bioB-Biotin Synthase
CPn1045	1199590	1198901	R	*conserved hypothetical bacterial membrane protein
CPn1046	1200675	1199590	R	*Tryptophan Hydroxylase
CPn1047	1200552	1201343	F	dapB-Dihydrodipicolinate Reductase-(CT364)
CPn1048	1201606	1202604	F	asd-Aspartate Dehydrogenase-(CT363)
CPn1049	1202595	1203914	F	lysC-Aspartokinase III-(CT362)
CPn1050	1203926	1204798	F	dapA-Dihydrodipicolinate Synthase-(CT361)
CPn1051	1204962	1205270	F	
CPn1052	1205417	1206169	F	
CPn1053	1206153	1206701	F	
CPn1054	1207034	1209466	F	
CPn1055	1209694	1210521	F	
CPn1056	1210527	1211228	F	
CPn1057	1211497	1213596	F	CT356 hypothetical protein
CPn1058	1213748	1214836	F	CT355 hypothetical protein
CPn1059	1214848	1215678	F	kgsA-Dimethyladenosine Transferase-(CT354)
CPn1060	1217658	1215727	R	dxe/tkt-Transketolase-(CT331)
CPn1061	1217920	1217666	R	CT330 hypothetical protein
CPn1062	1219820	1218159	R	xseA-Exodoxynucleoside VII-(CT329)
CPn1063	1219951	1220712	F	tpiS-Triosephosphate Isomerase-(CT328)

WO 00/27994

PCT/US99/26923

CPnl064	1220719	1220895	F	
CPnl065	1221095	1220928	R	
CPnl066	1221135	1221488	F	
CPnl067	1221735	1222292	F	def-Polypeptide Deformylase-(CT353)
CPnl068	1223258	1222365	R	rnhB_2-Ribonuclease HII_2-(CT008)
CPnl069	1223513	1223941	F	yfgA-HTH Transcriptional Regulator-(CT009)
CPnl070	1225511	1224144	R	
CPnl071	1227324	1225885	R	
CPnl072	1227969	1228835	F	
CPnl073	1229011	1229832	F	Predicted OMP_2 -(CT371)

WO 00/27994

PCT/US99/26923

Table 2 (Supplemental Data) Functional Assignments of *C. pneumoniae* Coding Sequences. *C. trachomatis* genes are shown in parentheses.

5			Amino Acid Biosynthesis
	<i>Aromatic Family</i>		
	1039 (CT366)	aroA	Phosphoshikimate Vinyltransferase
	1036 (CT369)	aroB	Dehydroquinate Synthase
	1037 (CT368)	aroC	Chorismate Synthase
10	1035 (CT370)	aroE	Shikimate 5-Dehydrogenase
	0484 (CT382)	aroG	Deoxyheptonate Aldolase
	1038 (CT367)	aroL	Shikimate Kinase II
	0740 (CT637)	tyrB	Aromatic AA Aminotransferase
	<i>Aspartate Family (lysine)</i>		
15	1048 (CT363)	asd	Aspartate Dehydrogenase
	1050 (CT361)	dapA	Dihydrodipicolinate Synthase
	1047 (CT364)	dapB	Dihydrodipicolinate Reductase
	0519 (CT430)	dapF	Dianinopimelate Epimerase
	1049 (CT362)	lysC	Aspartokinase III
20	<i>Serine Family</i>		
	0433 (CT282)	gcsH	Glycine Cleavage System H Protein
	0521 (CT432)	glyA	Serine Hydroxymethyltransferase
	<i>Base &amp; Nucleotide Metabolism</i>		
	0171	guaA	GMP Synthase
25	0172	guaB	Inosine 5'-Monophosphate Dehydrogenase
	0608		Uridine 5'-Monophosphate Synthase
	0735		Uridine Kinase
	0244 (CT128)	adk	Adenylate Kinase
	0894 (CT751)	amn	AMP Nucleosidase
30	0568 (CT452)	cmk	CMP Kinase
	0392 (CT039)	dcd	dCTP Deaminase
	0059 (CT292)	dut	dUTP Nucleotidohydrolase
	0120 (CT030)	gmK	GMP Kinase
	0619 (CT500)	ndk	Nucleoside-2-P Kinase
35	0984 (CT827)	nrdA	Ribonucleoside Reductase, Large Chain
	0985 (CT828)	nrdB	Ribonucleoside Reductase, Small Chain
	0236 (CT183)	pyrG	CTP Synthetase
	0698 (CT678)	pyrH	UMP Kinase
	0273 (CT188)	tdk	Thymidylate Kinase
40	0659 (CT539)	trxA	Thioredoxin
	0314 (CT099)	trxB	Thioredoxin Reductase
	1001 (CT844)	yfhC	Cytosine Deaminase
	<i>Biosynthesis of Cofactors</i>		
45	<i>Biotin, Lipote &amp; Ubiquinone</i>		
	1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
	1044	bioB	Biotin Synthase
	1042	bioD	Dethiobiotin Synthetase
	0923 (CT777)	bioF_1	Oxononanoate Synthase_1
50	1043 (CT777)	bioF_2	Oxononanoate Synthase_2
	0866 (CT725)	birA	Biotin Synthetase
	0748 (CT628)	ispA	Geranyl Transtransferase
	0832 (CT558)	lipA	Lipote Synthetase

WO 00/27994

PCT/US99/26923

	0265	(CT219)	ubiA	Benzoate Octaphenyltransferase
	0264	(CT220)	ubiD	Phenylacrylate Decarboxylase
	0515	(CT428)	ubiE	Ubiquinone Methyltransferase
	<i>Folic Acid</i>			
5	0759	(CT613)	folA	Dihydrofolate Reductase
	0335	(CT078)	folD	Methylene Tetrahydrofolate Dehydrogenase
	0758	(CT613)	folP	Dihydropterolate Synthase
	0757	(CT614)	folX	Dihydroneopterin Aldolase
	0763	(CT649)	ygfA	Formyltetrahydrofolate Cycloligase
10	<i>Porphyrin</i>			
	0714	(CT662)	hemA	Glutamyl tRNA Reductase
	0744	(CT633)	hemB	Porphobilinogen Synthase
	0052	(CT299)	hemC	Porphobilinogen Deaminase
	0890	(CT747)	hemE	Uroporphyrinogen Decarboxylase
15	0888	(CT745)	hemG	protoporphyrinogen Oxidase
	0138	(CT210)	hemL	Glutamate-1-Semialdehyde-2,1-Aminomutase
	0380	(CT052)	hemN_1	Coproporphyrinogen III Oxidase_1
	0889	(CT746)	hemN_2	Coproporphyrinogen III Oxidase_2
	0603	(CT485)	hemZ	Ferrochetalase
20	<i>Riboflavin</i>			
	0872	(CT731)	ribA&ribB	GTP Cyclohydrolase & DHBP Synthase
	0532	(CT405)	ribC	Riboflavin Synthase
	0871	(CT730)	ribD	Riboflavin Deaminase
	0873	(CT732)	ribE	Ribitylumazine Synthase
25	0320	(CT093)	ribF	FAD Synthase
	<i>Cell Envelope</i>			
	<i>Fatty Acid &amp; Phospholipid Metabolism</i>			
	0161	(CT206)		(predicted acyltransferase family)
30	0922	(CT776)	aas	Acylglycerophosphoethanolamine Acyltransferase
	0414	(CT265)	accA	AcCoA Carboxylase/Transferase Alpha
	0183	(CT123)	accB	Biotin Carboxyl Carrier Protein
	0182	(CT124)	accC	Biotin Carboxylase
	0058	(CT293)	accD	AcCoA Carboxylase/Transferase Beta
35	0295	(CT236)	acpP	Acyl Carrier Protein
	0313	(CT100)	acpS	Acyl-carrier Protein Synthase
	0567	(CT451)	cdsA	Phosphatidate Cytidyltransferase
	0297	(CT238)	fabD	Malonyl Acyl Carrier Transcyclase
	0916	(CT770)	fabF	Acyl Carrier Protein Synthase
40	0296	(CT237)	fabG	Oxoacyl (Carrier Protein) Reductase
	0298	(CT239)	fabH	Oxoacyl Carrier Protein Synthase III
	0406	(CT104)	fabI	Enoyl-Acyl-Carrier Protein Reductase
	0651	(CT532)	fabZ	Myristoyl-Acyl Carrier Dehydratase
	0098	(CT010)	htrB	Acyltransferase
45	0271	(CT136)		Lysophospholipase Esterase
	0615	(CT496)	pgsA_1	Glycerol-3-P Phosphatidyltransferase_1
	0947	(CT797)	pgsA_2	Glycerol-3-P Phosphatidyltransferase_2
	0958	(CT807)	plsB	Glycerol-3-P Acyltransferase
	0569	(CT453)	plsC	Glycerol-3-P Acyltransferase
50	0962	(CT811)	plsX	FA/Phospholipid Synthesis Protein
	0839	(CT699)	psdD	Phosphatidylserine Decarboxylase
	0983	(CT826)	pssA	Glycerol-Serine Phosphatidyltransferase
	0921	(CT775)		snGlycerol-3-P Acyltransferase
	0654	(CT535)	yciA	Acyl-CoA Thioesterase
55	0877	(CT736)	ybcL	CT736 Hypothetical Protein

LPS

WO 00/27994

PCT/US99/26923

	0154	(CT208)	gseA	KDO Transferase
	0721	(CT655)	kdsA	KDO Synthetase
	0235	(CT182)	kdsB	Deoxyoctulosonic Acid Synthetase
5	0650	(CT531)	lpxA	Acyl-Carrier UDP-GlcNAc O-Acyltransferase
	0965	(CT411)	lpxB	Lipid A Disaccharide Synthase
	0652	(CT533)	lpxC	Myristoyl GlcNAc Deacetylase
	0302	(CT243)	lpxD	UDP Glucosamine N-Acyltransferase
<i>Membrane Proteins, Lipoproteins &amp; Porins</i>				
10	0310	(CT251)	60IM	60kDa Inner Membrane Protein
	0556	(CT442)	crpA	15kDa Cysteine-Rich Protein
	0653	(CT534)	cutE	Apolipoprotein N-Acetyltransferase
	0311	(CT252)	lgt	Prolipoprotein Diacylglycerol Transferase
	0558	(CT444)	omcA	9kDa-Cysteine-Rich Lipoprotein
15	0557	(CT443)	omcB	60kDa Cysteine-Rich OMP
	0695	(CT681)	ompA	Major Outer Membrane Protein
	0854	(CT713)	ompB	Outer Membrane Protein B
	0781	(CT600)	pal	Peptidoglycan-Associated Lipoprotein
	0300	(CT241)	yaeT	Omp85 Homolog
<i>Peptidoglycan</i>				
20	0417	(CT268)	amiA	N-Acetylmuramoyl Alanine Amidase
	0780	(CT601)	amiB	N-Acetylmuramoyl-L-Ala Amidase
	0672	(CT551)	dacF	D-Ala-D-Ala Carboxypeptidase
	0968	(CT816)	glmS	Glucosamine-Fructose-6-P Aminotransferase
	0749	(CT629)	glmU	UDP-GlcNAc Pyrophosphorylase
25	0900	(CT757)	mraY	Muramoyl-Pentapeptide Transferase
	0571	(CT455)	murA	UDP-N-Acetylglucosamine Transferase
	0988	(CT831)	murB	UDP-N-Acetylenolpyruvoylglucosamine Reductase
	0905	(CT762)	murC&ddIA	Muramate-Ala Ligase & D-Ala-D-Ala Ligase
	0901	(CT758)	murD	Muramoylalanine-Glutamate Ligase
30	0418	(CT269)	murE	N-Acetylmuramoylalanylglutamyl DAP Ligase
	0899	(CT756)	murF	Muramoyl-DAP Ligase
	0904	(CT761)	murG	Peptidoglycan Transferase
	0902	(CT759)	nlpD	Muramidase (invasin repeat family)
	0694	(CT682)	pbp2	PBP2-Transglycolase/Transpeptidase
35	0419	(CT270)	pbp3	Transglycolase/Transpeptidase
	0421	(CT272)	yabC	PBP2B Family Methyltransferase
<i>Cellular Processes</i>				
<i>Cell Division</i>				
40	0959	(CT808)	cafE	Axial Filament Protein
	0880	(CT739)	ftsK	Cell Division Protein FtsK
	0903	(CT760)	ftsW	Cell Division Protein FtsW
	0972	(CT820)	ftsY	Cell Division Protein FtsY
	0617	(CT498)	gidA	FAD-dependent Oxidoreductase
45	0805	(CT582)	minD	Chromosome Partitioning ATPase
	0850	(CT709)	mreB	Rod Shape Protein-Sugar Kinase
	0867	(CT726)	rodA	Rod Shape Protein
	0684	(CT688)	parB	Chromosome Partitioning Protein
<i>Detoxification</i>				
50	0057	(CT294)	sodM	Superoxide Dismutase (Mn)
	0778	(CT603)	ahpC	Thio-specific Antioxidant (TSA) Peroxidase
<i>Signal Transduction</i>				
	0148	(CT145)		S/T Protein Kinase
	0584	(CT467)	atoS	Two-Component Sensor
55	0294	(CT235)		cAMP-Dependent Protein Kinase Regulatory Subunit
	0712	(CT664)		(FHA domain)

WO 00/27994

PCT/US99/26923

	0478	(CT379)	hflX	GTP Binding Protein
	0703	(CT673)		S/T Protein Kinase
	0095	(CT301)		S/T Protein Kinase
	0397	(CT259)		PP2C Phosphatase Family
5	0037	(CT337)	ptsH	PTS Phosphocarrier Protein Hpr
	0038	(CT336)	ptsI	PTS PEP Phosphotransferase
	0060	(CT291)	ptsN_1	PTS IIA Protein_1
	0061	(CT290)	ptsN_2	PTS IIA Protein + HTH DNA-Binding Domain
	0262	(CT218)	surE	SurE-like Acid Phosphatase
10	0838	(CT698)	thdF	Thiophene/Furan Oxidation Protein
	0693	(CT683)		TPR Repeats-CT683 Hypothetical Protein
	0321	(CT092)	ychF	GTP Binding Protein
	0544	(CT418)	yhbZ	GTP binding protein
	0844	(CT703)	yphC	GTPase/GTP-binding protein
15	<i>Standard Protein Secretion</i>			
	0115	(CT025)	fliH	Signal Recognition Particle GTPase
	0363	(CT060)	fliA	Flagellar Secretion Protein
	0858	(CT717)	fliI	Flagellum-specific ATP Synthase
	0704	(CT672)	fliN	Flagellar Motor Switch Domain/YacQ family
20	0815	(CT572)	gspD	Gen. Secretion Protein D
	0816	(CT571)	gspE	Gen. Secretion Protein E
	0817	(CT570)	gspF	Gen. Secretion Protein F
	0359	(CT064)	lcpA	GTPase
	0110	(CT020)	lepB	Signal Peptidase I
25	0535	(CT408)	lspA	Lipoprotein Signal Peptidase
	0260	(CT141)	secA_1	Protein Translocase Subunit_1
	0841	(CT701)	secA_2	Translocase SecA_2
	0564	(CT448)	secD&secF	Protein Export Proteins SecD/SecF (fusion)
	0075	(CT321)	secE	Preprotein Translocase
30	0629	(CT510)	secY	Translocase
	0848	(CT707)	tig	Trigger Factor-Peptidyl-prolyl Isomerase
	<i>Transport-Related Proteins</i>			
	0486			Hypothetical Proline Permease
	0289	(CT230)	aaaT	Neutral Amino Acid (Glutamate) Transporter
35	0691	(CT685)	abcX	ABC Transporter ATPase
	1031	(CT374)	arcD	Arginine/Omithine Antiporter
	0482	(CT381)	artJ	Arginine Periplasmic Binding Protein
	0836	(CT554)	brnQ	Amino Acid (Branched) Transport
	0536	(CT409)	dagA_1	D-Ala/Gly Permease_1
40	0876	(CT735)	dagA_2	D-Alanine/Glycine Permease_2
	0682	(CT690)	dppD	ABC ATPase Dipeptide Transport
	0683	(CT689)	dppF	ABC ATPase Dipeptide Transport
	0280	(CT689)	dppF	Dipeptide Transporter ATPase
	0785	(CT596)	exbB	Macromolecule Transporter
45	0784	(CT597)	exbD	Biopolymer Transport Protein
	0604	(CT486)	fliY	Glutamine Binding Protein
	0192	(CT129)	glnP	ABC Amino Acid Transporter Permease
	0191	(CT130)	glnQ	ABC Amino Acid Transporter ATPase
	0528	(CT401)	gltT	Glutamate Symport
50	0286	(CT194)	mgtE	Mg <sup>++</sup> Transporter (CBS Domain)
	0413	(CT264)	mabA	Transport ATP Binding Protein
	0290	(CT231)		Na <sup>+</sup> -dependent Transporter
	0195	(CT198)	oppA_1	Oligopeptide Binding Protein_1
	0196	(CT198)	oppA_2	Oligopeptide Binding Protein_2
55	0197	(CT139)	oppA_3	Oligopeptide Binding Protein_3
	0198	(CT175)	oppA_4	Oligopeptide Binding Protein_4

WO 00/27994

PCT/US99/26923

	0599	(CT480)	oppA_5	Oligopeptide Binding Lipoprotein_5
	0199	(CT199)	oppB_1	Oligopeptide Permease_1
	0598	(CT479)	oppB_2	Oligopeptide Permease_2
5	0200	(CT200)	oppC_1	Oligopeptide Permease_1
	0597	(CT478)	oppC_2	Oligopeptide Permease_2
	0201	(CT201)	oppD	Oligopeptide Transport ATPase
	0202	(CT202)	oppF	Oligopeptide Transport ATPase
	0231	(CT180)	tauB	ABC Transport ATPase (Nitrate/Fe)
	0782	(CT599)	tolB	Macromolecule Transporter
10	0969	(CT817)	tyrP_1	Tyrosine Transport_1
	0970	(CT818)	tyrP_2	Tyrosine Transport_2
	0665	(CT544)	uhpC	Hexosphosphate Transport
	0282	(CT216)	xasA	Amino Acid Transporter
	0207	(CT204)	ybhI	dicarboxylate Translocator
15	0971	(CT819)	yccA	Transport Permease
	0248	(CT152)	ycfV	ABC Transporter ATPase
	1014	(CT856)	ychM	Sulfate Transporter
	0736	(CT641)	ygeD	Efflux Protein
	0680	(CT692)	ygo4	Phosphate Permease
20	0723	(CT653)	yhbG	ABC Transporter ATPase
	0023	(CT348)	yjiK	ABC Transporter Protein ATPase
	0127	(CT034)	ytiF	Cationic Amino Acid Transporter
	0349	(CT067)	ytgA	Solute Protein Binding Family
	0348	(CT068)	ytgB	ABC transporter ATPase
25	0347	(CT069)	ytgC	Integral Membrane Protein
	0346	(CT070)	ytgD	Integral Membrane Protein
	1012	(CT854)	yzcB	ABC Transporter Permease
	0868	(CT727)	zntA	Metal Transport P-type ATPase
	0279			Possible ABC Transporter Permease Protein
30	0543	(CT417)		(Metal Transport Protein)
	0692	(CT684)		ABC Transporter
	0542	(CT416)		ABC Transporter ATPase
	0690	(CT686)		ABC Transporter Membrane Protein
	0541	(CT415)		solute binding protein
35	<i>Type-III Secretion</i>			
	0323	(CT090)	lcrD	Low Calcium Response D
	0324	(CT089)	lcrE	Low Calcium Response E
	0811	(CT576)	lcrH_1	Low Ca Response Protein H_1
	1021	(CT862)	lcrH_2	Low Calcium Response_2
40	0325	(CT088)	sysE	Secretion Chaperone
	0702	(CT674)	yscC	Yop C/Gen Secretion Protein D
	0828	(CT559)	yscJ	Yop Translocation J
	0826	(CT561)	yscL	Yop Translocation L
	0707	(CT669)	yscN	Yop N (Flagellar-Type ATPase)
45	0825	(CT562)	yscR	Yop Translocation R
	0824	(CT563)	yscS	YopS Translocation Protein
	0823	(CT564)	yscT	YopT Translocation T
	0322	(CT091)	yscU	Yop Translocation Protein U
50	<i>Central Intermediary Metabolism</i>			
	<i>Glycogen Metabolism</i>			
	0856	(CT715)		UDP-Glucose Pyrophosphorylase
	0948	(CT798)	glgA	Glycogen Synthase
	0475	(CT866)	glgB	Glucan Branching Enzyme
55	0607	(CT489)	glgC	Glucose-1-P Adenyltransferase
	0307	(CT248)	glgP	Glycogen Phosphorylase
	0388	(CT042)	glgX	Glycogen Hydrolase (debranching)

WO 00/27994

PCT/US99/26923

	0326	(CT087)	malQ	Glucanotransferase
	0851	(CT710)	pckA	Phosphoenolpyruvate Carboxykinase
	<i>Phosphorous &amp; Sulfur</i>			
5	0548	(CT435)	cysJ	Sulfite Reductase
	0920	(CT774)	cysQ	Sulfite Synthesis/Biphosphate Phosphatase
	0025	(CT346)	assA	Sulphohydrolase
	0918	(CT772)	ppa	Inorganic Pyrophosphatase
	<b>DNA Replication, Modification, Repair &amp; Recombination</b>			
10	<i>DNA Mismatch Repair</i>			
	0505			3-Methyladenine DNA Glycosylase
	0812	(CT575)	mutL	DNA Mismatch Repair
	0941	(CT792)	mutS	DNA Mismatch Repair
	0402	(CT107)	mutY	Adenine Glycosylase
15	0732	(CT625)	nfo	Endonuclease IV
	0837	(CT697)	nth	Endonuclease III
	<i>DNA Modification</i>			
	0596	(CT477)	ada	Methyltransferase
	0114	(CT024)	hemK	A/G-specific Methylase
20	0891	(CT748)	mfd	Transcription-Repair Coupling
	0620	(CT501)	ruvA	Holliday Junction Helicase
	0390	(CT040)	ruvB	Holliday Junction Helicase
	0621	(CT502)	ruvC	Crossover Junction Endonuclease
	0053	(CT298)	sms	Sms Protein
25	0773	(CT607)	ung	Uracil DNA Glycosylase
	1062	(CT329)	xseA	Exodeoxyribonuclease VII
	<i>DNA Recombination</i>			
	0762	(CT650)	recA	RecA Recombination Protein
	0738	(CT639)	recB	Exodeoxyribonuclease V, Beta
30	0737	(CT640)	recC	Exodeoxyribonuclease V, Gamma
	0123	(CT033)	recD_1	Exodeoxyribonuclease V (Alpha Subunit)_1
	0752	(CT652)	recD_2	Exodeoxyribonuclease V, Alpha_2
	0339	(CT074)	recF	ABC Superfamily ATPase
	0340	(CT074)		(frame-shift with 0339)
35	0563	(CT447)	recJ	ssDNA Exonuclease
	0299	(CT240)	recR	Recombination Protein
	<i>DNA Replication</i>			
	0309	(CT250)	dnaA_1	Replication Initiation Protein_1
	0424	(CT275)	dnaA_2	Replication Initiation Factor_2
40	0616	(CT497)	dnaB	Replicative DNA Helicase
	0666	(CT545)	dnaE	DNA Pol III Alpha
	0942	(CT794)	dnaG	DNA Primase
	0338	(CT075)	dnaN	DNA Pol III (Beta)
	0410	(CT261)	dnaQ_1	DNA Pol III Epsilon Chain_1
45	0655	(CT536)	dnaQ_2	DNA Pol III Epsilon Chain_2
	0040	(CT334)	dnaX_1	DNA Pol III Gamma and Tau_1
	0272	(CT187)	dnaX_2	DNA Pol III Gamma and Tau_2
	0149	(CT146)	dnI	DNA Ligase
	0274	(CT189)	gyrA_1	DNA Gyrase Subunit A_1
50	0716	(CT660)	gyrA_2	DNA Gyrase Subunit A_2
	0275	(CT190)	gyrB_1	DNA Gyrase Subunit B_1
	0715	(CT661)	gyrB_2	DNA Gyrase Subunit B_2
	0416	(CT267)	himD	Integration Host Factor Alpha
	0612	(CT493)	polA	DNA Polymerase I
55	0924	(CT778)	priA	Primosomal Protein N <sup>o</sup>
	0386	(CT044)	ssb	SS DNA Binding Protein



WO 00/27994

PCT/US99/26923

	0835 (CT355)	SWI/SNF family helicase_1
	0849 (CT708)	SWI/SNF family helicase_2
	0769 (CT643)	topA DNA Topoisomerase I-Fused to SWI Domain
	0024 (CT347)	xerC Integrase/recombinase
5	1024 (CT864)	xerD Integrase/recombinase
<i>Eukaryotic-Type Chromatin Factors</i>		
	0886 (CT743)	hctA Histone-Like Developmental Protein
	0384 (CT046)	hctB Histone-like Protein 2
	0878 (CT737)	SET Domain protein
10	0577 (CT460)	SWIB (YM74) Complex Protein
<i>UVR Exinuclease Repair System</i>		
	0096 (CT333)	uvrA Exinuclease ABC Subunit A
	0801 (CT586)	uvrB Exinuclease ABC Subunit B
	0940 (CT791)	uvrC Exinuclease ABC, Subunit C
15	0772 (CT608)	uvrD DNA Helicase
<i>Energy Metabolism</i>		
<i>Aerobic</i>		
	0855 (CT714)	gpdA Glycerol-3-P Dehydrogenase
20	0743 (CT634)	nqrA Ubiquinone Oxidoreductase, Alpha
	0427 (CT278)	nqr2 NADH (Ubiquinone) Dehydrogenase
	0428 (CT279)	nqr3 NADH (Ubiquinone) Oxidoreductase, Gamma
	0429 (CT280)	nqr4 NADH (Ubiquinone) Reductase 4
	0430 (CT281)	nqr5 NADH (Ubiquinone) Reductase 5
25	0883 (CT740)	nqr6 Phenolhydrolase/NADH (Ubiquinone) Oxidoreductase 6
<i>ATP Biogenesis and metabolism</i>		
	0351 (CT065)	adt_1 ADP/ATP Translocase_1
	0614 (CT495)	adt_2 ADP/ATP Translocase_2
	0088 (CT308)	atpA ATP Synthase Subunit A
30	0089 (CT307)	atpB ATP Synthase Subunit B
	0090 (CT306)	atpD ATP Synthase Subunit D
	0086 (CT310)	atpE ATP Synthase Subunit E
	0091 (CT305)	atpI ATP Synthase Subunit I
	0092 (CT304)	atpK ATP Synthase Subunit K
35	0860 (CT719)	flfF Flagellar M-Ring Protein
<i>Electron Transport Chain</i>		
	0102 (CT013)	cydA Cytochrome Oxidase Subunit I
	0103 (CT014)	cydB Cytochrome Oxidase Subunit II
	0364 (CT059)	Ferredoxin
40	0084 (CT312)	Predicted Ferredoxin
<i>Glycolysis &amp; Gluconeogenesis</i>		
	0281 (CT215)	dhnA Predicted 1,6-Fructose Biphosphate Aldolase
	0800 (CT587)	eno Enolase
	0624 (CT505)	gapA Glyceraldehyde-3-P Dehydrogenase
45	0056 (CT295)	musA Phosphomannomutase
	0967 (CT815)	pgm Phosphoglucomutase
	0160 (CT207)	pfkA_1 Fructose-6-P Phosphotransferase_1
	0208 (CT205)	pfkA_2 Fructose-6-P Phosphotransferase_2
	1025 (CT378)	pgi Glucose-6-P Isomerase
50	0679 (CT693)	pgk Phosphoglycerate Kinase
	0863 (CT722)	pgmA Phosphoglycerate Mutase
	0097 (CT332)	pyk Pyruvate Kinase
	1063 (CT328)	tpiS Triosephosphate Isomerase
<i>Pentose Phosphate Pathway</i>		
55	0239 (CT186)	devB Glucose-6-P Dehydrogenase (DevB family)
	1060 (CT331)	dxs Transketolase

WO 00/27994

PCT/US99/26923

	0360	(CT063)	gnd	6-Phosphogluconate Dehydrogenase
	0185	(CT121)	rpe	Ribulose-P Epimerase
	0141	(CT213)	rpiA	Ribose-5-P Isomerase A
	0083	(CT313)	tal	Transaldolase
5	0893	(CT750)	tktB	Transketolase
	0238	(CT185)	zwf	Glucose-6-P Dehydrogenase
	<i>Pyruvate Dehydrogenase</i>			
	0833	(CT557)	lpdA	Lipoamide Dehydrogenase
10	0436	(CT285)	lplA_1	Lipoate Protein Ligase-Like Protein
	0618	(CT499)	lplA_2	Lipoate-Protein Ligase A
	0033	(CT340)	pdhA&B	Oxoisovalerate Dehydrogenase $\alpha/\beta$ Fusion
	0304	(CT245)	pdhA	Pyruvate Dehydrogenase Alpha
	0305	(CT246)	pdhB	Pyruvate Dehydrogenase Beta
	0306	(CT247)	pdhC	Dihydrolipoamide Acetyltransferase
15	<i>TCA Cycle</i>			
	0495	(CT390)	aspC	Aspartate Aminotransferase
	1013	(CT855)	fumC	Fumarate Hydratase
	1028	(CT376)	mdhC	Malate Dehydrogenase
	0789	(CT592)	sdhA	Succinate Dehydrogenase
20	0790	(CT591)	sdhB	Succinate Dehydrogenase
	0788	(CT593)	sdhC	Succinate Dehydrogenase
	0378	(CT054)	sucA	Oxoglutarate Dehydrogenase
	0377	(CT055)	sucB_1	Dihydrolipoamide Succinyltransferase_1
	0527	(CT400)	sucB_2	Dihydrolipoamide Succinyltransferase_2
25	0973	(CT821)	sucC	Succinyl-CoA Synthetase, Beta
	0974	(CT822)	sucD	Succinyl-CoA Synthetase, Alpha
	<i>Protein Folding, Assembly &amp; Modification</i>			
	<i>Chaperones</i>			
30	0949	(CT799)	ctc	General Stress Protein
	0534	(CT407)	dksA	DnaK Suppressor
	0032	(CT341)	dnaJ	Heat Shock Protein J
	0503	(CT396)	dnaK	Hsp-70
	0134	(CT110)	groEL_1	Hsp-60_1
35	0777	(CT604)	groEL_2	Hsp-60_2
	0898	(CT755)	groEL_3	Hsp-60_3
	0135	(CT111)	groES	10KDa Chaperonin
	0502	(CT395)	grpE	HSP-70 Cofactor
	0661	(CT541)	mip	FKBP-type Peptidyl-prolyl Cis-Trans Isomerase
40	<i>Proteases</i>			
	0144	(CT113)	clpB	Clp Protease ATPase
	0437	(CT286)	clpC	ClpC Protease
	0520	(CT431)	clpP_1	CLP Protease
	0847	(CT706)	clpP_2	CLP Protease Subunit
45	0846	(CT705)	clpX	CLP Protease ATPase
	0269	(CT138)		Dipeptidase
	0998	(CT841)	ftsH	ATP-dependent Zinc Protease
	0030	(CT343)	gcp_1	O-Sialoglycoprotein Endopeptidase_1
	0194	(CT197)	gcp_2	O-Sialoglycoprotein Endopeptidase_2
50	0979	(CT823)	htrA	DO Serine Protease
	0957	(CT806)	ide	Insulinase family/Protease III
	0027	(CT344)	lon	Lon ATP-dependent Protease
	1017	(CT859)	lytB	Metalloprotease
	1009	(CT851)	map	Methionine Aminopeptidase
55	0385	(CT045)	pepA	Leucyl Aminopeptidase A
	0136	(CT112)	pepF	Oligopeptidase

WO 00/27994

PCT/US99/26923

	0813	(CT574)	pepP	Aminopeptidase P
	0613	(CT494)	sohB	Protease
	0555	(CT441)	tsp	Tail-Specific Protease
	0344	(CT072)	yaeL	Metalloprotease
5	0981	(CT824)		Zinc Metalloprotease (insulinase family)
	<i>Protein Isomerases</i>			
	0227	(CT176)	dsbB	Disulfide bond Oxidoreductase
	0786	(CT595)	dsbD	Thio:disulfide Interchange Protein
	0228	(CT177)	dsbG	Disulfide Bond Chaperone
10	0933	(CT783)		Predicted Disulfide Bond Isomerase
	0926	(CT780)		Thioredoxin Disulfide Isomerase

WO 00/27994

PCT/US99/26923

## Transcription

## RNA Degradation

5	0999 (CT842)	pnp	Polyribonucleotide Nucleotidyltransferase
	0054 (CT297)	rnc	Ribonuclease III
	0119 (CT029)	rnH1_1	Ribonuclease HII_1
	1068 (CT008)	rnH2_2	Ribonuclease HII_2
	0934 (CT784)	rnpA	Ribonuclease P Protein Component
	0504 (CT397)	vacB	Ribonuclease Family

## 10 RNA Elongation &amp; Termination Factors

	0741 (CT636)	greA	Transcription Elongation Factor
	0316 (CT097)	nusA	N Utilization Protein A
	0076 (CT320)	nusG	Transcriptional Antitermination
	0845 (CT704)	pcnB_1	Poly A Polymerase_1
15	0966 (CT410)	pcnB_2	PolyA Polymerase_2
	0610 (CT491)	rho	Transcription Termination Factor

## RNA Methylases

	0674 (CT553)	fmu	RNA Methyltransferase
	1059 (CT354)	kgsA	Dimethyladenosine Transferase
20	0187 (CT133)		Predicted Methylase
	0530 (CT403)	spoU_1	rRNA Methylase_1
	0660 (CT540)	spoU_2	rRNA Methylase_2
	0117 (CT027)	trmD	tRNA (Guanine N-1)-Methyltransferase
	0885 (CT742)	ygcA	rRNA Methyltransferase
25	0986 (CT829)	yggH	Predicted rRNA Methylase
	0987 (CT830)	ytgB	Predicted rRNA Methylase

## RNA Modification

	0649 (CT530)	fmt	Methionyl tRNA Formyltransferase
	0910 (CT766)	miaA	tRNA Pyrophosphate Transferase
30	0719 (CT658)	sflB	Predicted Pseudouridine Synthase
	0219 (CT193)	tgt	Queuine tRNA Ribosyl Transferase
	0580 (CT463)	truA	Pseudouridylylase Synthase I
	0319 (CT094)	truB	tRNA Pseudouridine Synthase
	0403 (CT106)	yccC	Predicted Pseudouridine Synthetase Family
35	0864 (CT723)	yjbc	Predicted Pseudouridine Synthase

## RNA Polymerase &amp; Transcription Regulators

	0586 (CT468)	atoC	Two-Component Regulator
	0362 (CT061)	rpsD	Sigma-28/WhiG Family
	0501 (CT394)	hrcA	HTH Transcriptional Repressor
40	0793 (CT588)	rbsU	Sigma Regulatory Family Protein—PP2C Phosphatase (RsbW Antagonist)
	0626 (CT507)	rpoA	RNA Polymerase Alpha
	0081 (CT315)	rpoB	RNA Polymerase Beta
	0082 (CT314)	rpoC	RNA Polymerase Beta'
	0756 (CT615)	rpoD	RNA Polymerase Sigma-66
45	0771 (CT609)	rpoN	RNA Polymerase Sigma-54
	0511 (CT424)	rsbV_1	Sigma Regulatory Factor_1
	0909 (CT765)	rsbV_2	Sigma Factor Regulator_2
	0670 (CT549)	rsbW	Sigma Regulatory Factor-Histidine Kinase
	0750 (CT630)	tcID	HTH Transcriptional Regulatory Protein + Receiver Domain
50	1069 (CT009)	yfgA	HTH Transcriptional Regulator

## Translation

## Amino Acyl tRNA Synthesis

	0892 (CT749)	alaS	Alanyl tRNA Synthetase
55	0570 (CT454)	argS	Arginyl tRNA Transferase
	0662 (CT542)	aspS	Aspartyl tRNA Synthetase

WO 00/27994

PCT/US99/26923

	0932 (CT782)	cysS	Cysteinyl tRNA Synthetase
	0003 (CT003)	gatA	Glu tRNA Gln Amidotransferase (A subunit)
	0004 (CT004)	gatB	Glu tRNA Gln Amidotransferase (B Subunit)
	0002 (CT002)	gatC	Glu tRNA Gln Amidotransferase (C subunit)
5	0560 (CT445)	gluX	Glutamyl-tRNA Synthetase
	0946 (CT796)	glyQ	Glycyl tRNA Synthetase
	0663 (CT543)	hisS	Histidyl tRNA Synthetase
	0109 (CT019)	ileS	Isoleucyl-tRNA Synthetase
	0153 (CT209)	leuS	Leucyl tRNA Synthetase
10	0931 (CT781)	lysS	Lysyl tRNA Synthetase
	0122 (CT032)	metG	Methionyl-tRNA Synthetase
	0993 (CT836)	pheS	Phenylalanyl tRNA Synthetase, Alpha
	0594 (CT475)	pheT	Phenylalanyl tRNA Synthetase Beta
	0500 (CT393)	proS	Prolyl tRNA Synthetase
15	0870 (CT729)	serS	Seryl tRNA Synthetase_2
	0806 (CT581)	thrS	Threonyl tRNA Synthetase
	0802 (CT585)	trpS	Tryptophanyl tRNA Synthetase
	0361 (CT062)	tyrS	Tyrosyl tRNA Synthetase
	0094 (CT302)	valS	Valyl tRNA Synthetase
20	<i>Peptide Chain Initiation, Elongation &amp; Termination</i>		
	1067 (CT353)	def	Polypeptide Deformylase
	0184 (CT122)	efp_1	Elongation Factor P_1
	0895 (CT752)	efp_2	Elongation Factor P_2
	0550 (CT437)	fusA	Elongation Factor G
25	0073 (CT323)	infA	Initiation Factor IF-1
	0317 (CT096)	infB	Initiation Factor-2
	0990 (CT833)	infC	Initiation Factor 3
	0113 (CT023)	pfrA	Peptide Chain Releasing Factor 1
	0576 (CT459)	prfB	Peptide Chain Release Factor 2
30	0950 (CT800)	pth	Peptidyl tRNA Hydrolase
	0318 (CT095)	rbfA	Ribosome Binding Factor A
	0699 (CT677)	rnf	Ribosome Releasing Factor
	0697 (CT679)	tsf	Elongation Factor TS
	0074 (CT322)	tufA	Elongation Factor Tu
35	<i>Ribosomal Proteins</i>		
	0078 (CT318)	r11	L1 Ribosomal Protein
	0644 (CT525)	r12	L2 Ribosomal Protein
	0647 (CT528)	r13	L3 Ribosomal Protein
	0646 (CT527)	r14	L4 Ribosomal Protein
40	0635 (CT516)	r15	L5 Ribosomal Protein
	0633 (CT514)	r16	L6 Ribosomal Protein
	0080 (CT316)	r17	L7/L12 Ribosomal Protein
	0953 (CT803)	r19	L9 Ribosomal Protein
	0079 (CT317)	r110	L10 Ribosomal Protein
45	0077 (CT319)	r111	L11 Ribosomal Protein
	0247 (CT125)	r113	L13 Ribosomal Protein
	0637 (CT518)	r114	L14 Ribosomal Protein
	0630 (CT511)	r115	L15 Ribosomal Protein
	0640 (CT521)	r116	L16 Ribosomal Protein
50	0625 (CT506)	r117	L17 Ribosomal Protein
	0632 (CT513)	r118	L18 Ribosomal Protein
	0118 (CT028)	r119	L19 Ribosomal Protein
	0992 (CT835)	r120	L20 Ribosomal Protein
	0546 (CT420)	r121	L21 Ribosomal Protein
55	0642 (CT523)	r122	L22 Ribosomal Protein
	0645 (CT526)	r123	L23 Ribosomal Protein

WO 00/27994

PCT/US99/26923

5	0636	(CT517)	r124	L24 Ribosomal Protein
	0545	(CT419)	r127	L27 ribosomal protein
	0327	(CT086)	r128	L28 Ribosomal Protein
	0639	(CT520)	r129	L29 Ribosomal Protein
	0112	(CT022)	r131	L31 Ribosomal Protein
	0961	(CT810)	r132	L32 Ribosomal Protein
	0250	(CT150)	r133	L33 Ribosomal Protein
	0935	(CT785)	r134	L34 Ribosomal Protein
	0991	(CT834)	r135	L35 Ribosomal Protein
10	0936	(CT786)	r136	L36 Ribosomal Protein
	0315	(CT098)	rs1	S1 Ribosomal Protein
	0696	(CT680)	rs2	S2 Ribosomal Protein
	0641	(CT522)	rs3	S3 Ribosomal Protein
	0733	(CT626)	rs4	S4 Ribosomal Protein
15	0631	(CT512)	rs5	S5 Ribosomal Protein
	0951	(CT801)	rs6	S6 Ribosomal Protein
	0551	(CT438)	rs7	S7 Ribosomal Protein
	0634	(CT515)	rs8	S8 Ribosomal Protein
	0246	(CT126)	rs9	S9 Ribosomal Protein
20	0549	(CT436)	rs10	S10 Ribosomal Protein
	0627	(CT508)	rs11	S11 Ribosomal Protein
	0552	(CT439)	rs12	S12 Ribosomal Protein
	0628	(CT509)	rs13	S13 Ribosomal Protein
	0937	(CT787)	rs14	S14 Ribosomal Protein
25	1000	(CT843)	rs15	S15 Ribosomal Protein
	0116	(CT026)	rs16	S16 Ribosomal Protein
	0638	(CT519)	rs17	S17 Ribosomal Protein
	0952	(CT802)	rs18	S18 Ribosomal Protein
	0643	(CT524)	rs19	S19 Ribosomal Protein
30	0754	(CT617)	rs20	S20 Ribosomal Protein
	0031	(CT342)	rs21	S21 Ribosomal Protein

35

## Other Categories

*Chlamydia-Specific Proteins*

	0561	(CT446)	Euo	CHLPS Euo Protein
	0804	(CT583)	Gp6D	CHLTR Plasmid Paralog
	0186	(CT119)		Similarity to IncA_1
40	0291	(CT232)	incB	Inclusion Membrane Protein B
	0292	(CT233)	incC	Inclusion Membrane Protein C
	1026	(CT377)		LtaA Protein
	0333	(CT080)		LtaB Protein
	0005	(CT871)	pmp_1	Polymorphic Outer Membrane Protein G Family
45	0013	(CT871)	pmp_2	Polymorphic Outer Membrane Protein G Family
	0014	(CT871)	pmp_3	Polymorphic Outer Membrane Protein G Family
	0015	(CT871)	pmp_3	PMP_3 (frame-shift with 0014)
	0016	(CT874)	pmp_4	Polymorphic Outer Membrane Protein G Family
	0017	(CT871)	pmp_4	PMP_4 (frame-shift with 0016)
50	0018	(CT874)	pmp_5	Polymorphic Outer Membrane Protein G Family
	0019	(CT871)	pmp_5	PMP_5 (frame-shift with 0018)
	0444	(CT871)	pmp_6	Polymorphic Outer Membrane Protein G/I Family
	0445	(CT871)	pmp_7	Polymorphic Outer Membrane Protein G Family
	0446	(CT871)	pmp_8	Polymorphic Outer Membrane Protein G Family
55	0447	(CT871)	pmp_9	Polymorphic Outer Membrane Protein G/I Family
	0450	(CT871)	pmp_10	Polymorphic Outer Membrane Protein G Family
	0449	(CT871)	pmp_10	PMP_10 (Frame-shift with 0450)

WO 00/27994

PCT/US99/26923

	0451 (CT871)	pmp_11	Polymorphic Outer Membrane Protein G Family
	0452 (CT874)	pmp_12	Polymorphic Outer Membrane Protein (truncated) A/I Family
	0453 (CT871)	pmp_13	Polymorphic Outer Membrane Protein G Family
5	0454 (CT872)	pmp_14	Polymorphic Outer Membrane Protein H Family
	0466 (CT869)	pmp_15	Polymorphic Outer Membrane Protein E Family
	0467 (CT869)	pmp_16	Polymorphic Outer Membrane Protein E Family
	0468 (CT869)	pmp_17	Polymorphic Outer Membrane Protein E Family
	0469 (CT869)	pmp_17	PMP_17 (Frame-shift with 0468)
	0470 (CT869)	pmp_17	PMP_17 (Frame-shift with 0469)
10	0471 (CT870)	pmp_18	Polymorphic Outer Membrane Protein E/F Family
	0539 (CT412)	pmp_19	Polymorphic Membrane Protein A Family
	0540 (CT413)	pmp_20	Polymorphic Membrane Protein B Family
	0963 (CT812)	pmp_21	Polymorphic Membrane Protein D Family
15	0562		CHLPS 43 kDa Protein Homolog_1
	0927		CHLPS 43 kDa Protein Homolog_2
	0928		CHLPS 43 kDa Protein Homolog_3
	0929		CHLPS 43 kDa Protein Homolog_4
	0728 (CT622)		CHLPS 76kDa Homolog_1 (CT622)
	0729 (CT623)		CHLPS 76kDa Homolog_2 (CT623)
20	0133 (CT109)		CHLPS Hypothetical Protein
	0332 (CT081)		CHLPS T2 Protein

*Miscellaneous Enzymes/Conserved Proteins*

	0193	argR	Possible Arginine Repressor
	1046		Aromatic Amino Acid Hydroxylase
25	0232		Similarity to 5'-Methylthioadenosine Nucleosidase
	0128 (CT035)		Biotin Protein Ligase
	0513 (CT426)		Fe-S Oxidoreductase_1
	0911 (CT767)		Fe-S Oxidoreductase_2
	0373 (CT057)	gcpE	GcpE Protein
30	0407 (CT103)		HAD Superfamily Hydrolase/Phosphatase
	0917 (CT771)		Hydrolase/Phosphatase Homolog
	0488 (CT385)	ycfF	HIT Family Hydrolase
	0701 (CT675)	karG	Arginine Kinase
	0526 (CT399)	kpsF	GutQ/KpsF Family Sugar-P Isomerase
35	0919 (CT773)	ldh	Leucine Dehydrogenase
	0022 (CT349)	maf	Maf protein
	0997 (CT840)	mesJ	PP-loop superfamily ATPase
	0151 (CT148)	mhpA	Monoxygenase
	0730 (CT624)	mviN	Integral Membrane Protein
40	0861 (CT720)		NifU-Related Protein
	0479 (CT380)	phnP	Metal Dependent Hydrolase
	0106 (CT015)	phoH	ATPase
	0329 (CT084)		Phospholipase D Superfamily
	0435 (CT284)		Phospholipase D Superfamily
45	0581 (CT464)		Phosphoglycolate Phosphatase
	0897 (CT754)		Predicted Phosphohydrolase
	0509 (CT422)		Predicted Metalloenzyme
	1030 (CT375)		Predicted D-Amino Acid Dehydrogenase
	0531 (CT404)		SAM Dependent Methyltransferase
50	0337 (CT076)	smgB	Small Protein B
	0394 (CT256)	tlc_1	CBS Domain Protein (Hemolysin Homolog)_1
	0510 (CT423)	tlc_2	CBS Domains (Hemolysin Homolog)_2
	0382 (CT048)	yabC	SAM-Dependent Methyltransferase
	0787 (CT594)	yabD	PHP Superfamily (Urease/Pyrimidinase) Hydrolase
55	0611 (CT492)	yacE	Predicted Phosphatase/Kinase
	0579 (CT462)	yacM	Sugar Nucleotide Phosphorylase
	0578 (CT461)	yacI	Phosphohydrolase

WO 00/27994

PCT/US99/26923

	0345	(CT071)	yaeM	CT071 Hypothetical Protein
	0566	(CT450)	yaeS	YaeS family Hypothetical Protein
	0591	(CT472)	yagE	YagE family
5	0039	(CT335)	ybaB	YbaB family Hypothetical Protein
	0101	(CT012)	ybbP	YbbP family Hypothetical Protein
	0915	(CT769)	ybeB	iojap Superfamily Ortholog
	0137	(CT108)	ybgI	ACR family
	0529	(CT402)	ycaH	ATPase
10	0438	(CT287)	ycbF	PP-loop Superfamily ATPase
	0734	(CT627)	yceA	YceA Hypothetical Protein
	0954	(CT804)	ychB	Predicted Kinase
	0261	(CT217)	ydaO	PP-Loop Superfamily ATPase
	0245	(CT127)	ydhO	Polysaccharide Hydrolase-Invasin Repeat Family
	0573	(CT457)	yebC	YebC Family Hypothetical Protein
15	0689	(CT687)	yfhO_1	NifS-related Aminotransferase_1
	0862	(CT721)	yfhO_2	NifS-related Aminotransferase_2
	0547	(CT434)	ygbB	YgbB Family Hypothetical Protein
	0237	(CT184)	yggF	YggF Family Hypothetical Protein
	0775	(CT606)	yggV	YggV Family Hypothetical Protein
20	0396	(CT258)	yhfO_3	NifS-related Aminotransferase_3
	0605	(CT487)	yhhF	Predicted Methylase
	0575	(CT458)	yhhY	Amino Group Acetyl Transferase
	0592	(CT473)	yidD	YidD Family
	0982	(CT825)	yigN	YigN Family Hypothetical Protein
25	0657	(CT537)	yjeE	YjeE Hypothetical Protein
	0768	(CT644)	yohI	YohI Predicted Oxidoreductase
	0336	(CT077)	yojL	YojL Hypothetical Protein
	0217	(CT140)	ypdP	YpdP Hypothetical Protein
	0140	(CT212)	yqdE	YqdE Hypothetical Protein
30	0263	(CT221)	yqfU	YqfU Hypothetical Protein
	0139	(CT211)	yqgE	YqgE Hypothetical Protein
	0270	(CT137)	ywlC	SuA5 Superfamily-related Protein
	0879	(CT738)	yyeJ	Metal Dependent Hydrolase
35				Homologs to CHLTR Hypothetical Coding Genes
	0001	(CT001)	CT001	Hypothetical Protein
	0020	(CT351)	CT351	Hypothetical Protein
	0021	(CT350)	CT350	Hypothetical Protein
40	0026	(CT345)	CT345	Hypothetical Protein
	0035	(CT339)	CT339	Hypothetical Protein
	0036	(CT338)	CT338	Hypothetical Protein
	0055	(CT296)	CT296	Hypothetical Protein
	0062	(CT289)	CT289	Hypothetical Protein
	0065	(CT288)	CT288	Hypothetical Protein
45	0068	(CT360)	CT360	Hypothetical Protein
	0071	(CT325)	CT325	Hypothetical Protein
	0072	(CT324)	CT324	Hypothetical Protein
	0085	(CT311)	CT311	Hypothetical Protein
	0087	(CT309)	CT309	Hypothetical Protein
50	0093	(CT303)	CT303	Hypothetical Protein
	0100	(CT011)	CT011	Hypothetical Protein
	0104	(CT017)	CT017	Hypothetical Protein
	0105	(CT016)	CT016	Hypothetical Protein
	0107	(CT058)	CT058	Hypothetical Protein_1
55	0108	(CT018)	CT018	Similarity
	0111	(CT021)	CT021	Hypothetical Protein
	0121	(CT031)	CT031	Hypothetical Protein



WO 00/27994

PCT/US99/26923

	0129	(CT036)	CT036 Similarity
	0145	(CT114)	CT114 Hypothetical Protein
	0150	(CT147)	CT147 Hypothetical Protein
	0152	(CT149)	CT149 Hypothetical Protein
5	0176	(CT153)	CT153 Hypothetical Protein
	0188	(CT132)	CT132 Hypothetical Protein
	0189	(CT131)	CT131 Hypothetical Protein
	0206	(CT203)	CT203 Hypothetical Protein
	0229	(CT178)	CT178 Hypothetical Protein
10	0230	(CT179)	CT179 Hypothetical Protein
	0234	(CT181)	CT181 Hypothetical Protein
	0249	(CT151)	CT151 Hypothetical Protein
	0253	(CT144)	CT144 Hypothetical Protein_1
	0254	(CT143)	CT143 Hypothetical Protein_1
15	0255	(CT142)	CT142 Hypothetical Protein_1
	0256	(CT144)	CT144 Hypothetical Protein_2
	0257	(CT143)	CT143 Hypothetical Protein_2
	0259	(CT142)	CT142 Hypothetical Protein_2
	0276	(CT191)	CT191 Hypothetical Protein
20	0288	(CT195)	CT195 Hypothetical Protein
	0293	(CT234)	CT234 Hypothetical Protein
	0301	(CT242)	CT368 Hypothetical Protein
	0303	(CT244)	CT244 Hypothetical Protein
	0308	(CT249)	CT249 Similarity
25	0312	(CT101)	CT101 Hypothetical Protein
	0328	(CT085)	CT085 Hypothetical Protein
	0330	(CT083)	CT083 Hypothetical Protein
	0331	(CT082)	CT082 Hypothetical Protein
	0334	(CT079)	CT079 Similarity
30	0342	(CT073)	CT073 Hypothetical Protein
	0343	(CT073)	(frame-shift with 0342?)
	0350	(CT066)	CT066 Hypothetical Protein
	0369	(CT058)	CT058 Hypothetical Protein_2
	0370	(CT058)	CT058 Hypothetical Protein_3
35	0374	(CT056)	CT056 Hypothetical Protein
	0379	(CT053)	CT053 Hypothetical Protein
	0381	(CT326)	CT326 Similarity
	0383	(CT047)	CT047 Hypothetical Protein
	0387	(CT043)	CT043 Hypothetical Protein
40	0389	(CT041)	CT041 Hypothetical Protein
	0393	(CT038)	CT038 Hypothetical Protein
	0395	(CT257)	CT257 Hypothetical Protein
	0399	(CT253)	CT253 Hypothetical Protein
	0400	(CT254)	CT254 Hypothetical Protein
45	0401	(CT255)	CT255 Hypothetical Protein
	0405	(CT105)	CT105 Hypothetical Protein
	0408	(CT102)	CT102 Hypothetical Protein
	0409	(CT260)	CT260 Hypothetical Protein
	0411	(CT262)	CT262 Hypothetical Protein
50	0412	(CT263)	CT263 Hypothetical Protein
	0415	(CT266)	CT266 Hypothetical Protein
	0420	(CT271)	CT271 Hypothetical Protein
	0422	(CT273)	CT273 Hypothetical Protein
	0423	(CT274)	CT274 Hypothetical Protein
55	0425	(CT276)	CT276 Hypothetical Proteins
	0426	(CT277)	CT277 Similarity
	0434	(CT283)	CT283 Hypothetical Protein

WO 00/27994

PCT/US99/26923

	0441	(CT007)	CT007 Hypothetical Protein
	0442	(CT006)	CT006 Hypothetical Protein
	0443	(CT005)	CT005 Hypothetical Protein
	0474	(CT365)	CT365 Hypothetical Protein
5	0476	(CT865)	CT865 Hypothetical Protein
	0480	(CT383)	CT383 Hypothetical Protein
	0485	(CT382)	CT382.1 Hypothetical Protein
	0487	(CT384)	CT384 Hypothetical Protein
	0489	(CT386)	CT386 Hypothetical Protein
10	0490	(CT387)	CT387 Hypothetical Protein
	0491	(CT389)	CT389 Hypothetical Protein
	0496	(CT391)	CT391 Hypothetical Protein
	0497	(CT388)	CT388 Hypothetical Protein
	0506	(CT421)	CT421 Hypothetical Protein
15	0507	(CT421)	CT421.1 Hypothetical Protein
	0508	(CT421)	CT421.2 Hypothetical Protein
	0512	(CT425)	CT425 Hypothetical Protein
	0514	(CT427)	CT427 Hypothetical Protein
	0518	(CT429)	CT429 Hypothetical Protein
20	0522	(CT433)	CT433 Hypothetical Protein
	0525	(CT398)	CT398 Hypothetical Protein
	0533	(CT406)	CT406 Hypothetical Protein
	0537	(CT814)	CT814.1 Hypothetical Protein
	0538	(CT814)	CT814 Hypothetical Protein
25	0554	(CT440)	CT440 Hypothetical Protein
	0559	(CT441)	CT441.1 Hypothetical Protein
	0565	(CT449)	CT449 Hypothetical Protein
	0572	(CT456)	CT456 Hypothetical Protein
	0582	(CT465)	CT465 Hypothetical Protein
30	0583	(CT466)	CT466 Hypothetical Protein
	0588	(CT469)	CT469 Hypothetical Protein
	0589	(CT470)	CT470 Hypothetical Protein
	0590	(CT471)	CT471 Hypothetical Protein
	0593	(CT474)	CT474 Hypothetical Protein
35	0595	(CT476)	CT476 Hypothetical Protein
	0601	(CT483)	CT483 Hypothetical Protein
	0602	(CT484)	CT484 Hypothetical Protein
	0606	(CT488)	CT488 Hypothetical Protein
	0609	(CT490)	CT490 Hypothetical Protein
40	0622	(CT503)	CT503 Hypothetical Protein
	0623	(CT504)	CT504 Hypothetical Protein
	0648	(CT529)	CT529 Hypothetical Protein
	0658	(CT538)	CT538 Hypothetical Protein
	0667	(CT546)	CT546 Hypothetical Protein
45	0668	(CT547)	CT547 Hypothetical Protein
	0669	(CT548)	CT548 Hypothetical Protein
	0671	(CT550)	CT550 Hypothetical Protein
	0673	(CT552)	CT552 Hypothetical Protein
	0675	(CT696)	CT696 Hypothetical Protein
50	0676	(CT695)	CT695 Similarity
	0681	(CT691)	CT691 Hypothetical Protein
	0687	(CT482)	CT482 Hypothetical Protein
	0688	(CT481)	CT481 Hypothetical Protein
	0700	(CT676)	CT676 Hypothetical Protein
55	0705	(CT671)	CT671 Hypothetical Protein
	0706	(CT670)	CT670 Hypothetical Protein
	0708	(CT668)	CT668 Hypothetical Protein

WO 00/27994

PCT/US99/26923

	0709 (CT667)	CT667 Hypothetical Protein
	0710 (CT666)	CT666 Hypothetical Protein
	0711 (CT665)	CT665 Hypothetical Protein
	0713 (CT663)	CT663 Hypothetical Protein
5	0717 (CT656)	CT656 Hypothetical Protein
	0718 (CT657)	CT657 Hypothetical Protein
	0720 (CT659)	CT659 Hypothetical Protein
	0722 (CT654)	CT654 Hypothetical Protein
	0725 (CT652)	CT652.1 Hypothetical Protein
10	0726 (CT620)	CT620 Hypothetical Protein
	0727 (CT619)	CT619 Hypothetical Protein
	0739 (CT638)	CT638 Hypothetical Protein
	0742 (CT635)	CT635 Hypothetical Protein
	0746 (CT632)	CT632 Hypothetical Protein
15	0747 (CT631)	CT631 Hypothetical Protein
	0751 (CT651)	CT651 Hypothetical Protein
	0755 (CT616)	CT616 Hypothetical Protein
	0760 (CT611)	CT611 Hypothetical Protein
	0761 (CT610)	CT610 Hypothetical Protein
20	0764 (CT648)	CT648 Hypothetical Protein
	0765 (CT647)	CT647 Hypothetical Protein
	0766 (CT646)	CT646 Hypothetical Protein
	0767 (CT645)	CT645 Hypothetical Protein
	0770 (CT642)	CT642 Hypothetical Protein
25	0774 (CT606)	CT606.1 Hypothetical Protein
	0776 (CT605)	CT605 Hypothetical Protein
	0779 (CT602)	CT602 Hypothetical Protein
	0783 (CT598)	CT598 Hypothetical Protein
	0791 (CT590)	CT590 Hypothetical Protein
30	0792 (CT589)	CT589 Hypothetical Protein
	0803 (CT584)	CT584 Hypothetical Protein
	0807 (CT580)	CT580 Hypothetical Protein
	0808 (CT579)	CT579 Hypothetical Protein
	0809 (CT578)	CT578 Hypothetical Protein
35	0810 (CT577)	CT577 Hypothetical Protein
	0814 (CT573)	CT573 Hypothetical Protein
	0818 (CT569)	CT569 Hypothetical Protein
	0819 (CT568)	CT568 Hypothetical Protein
	0820 (CT567)	CT567 Hypothetical Protein
40	0821 (CT566)	CT566 Hypothetical Protein
	0822 (CT565)	CT565 Hypothetical Protein
	0827 (CT560)	CT560 Hypothetical Protein
	0834 (CT556)	CT556 Hypothetical Protein
	0840 (CT700)	CT700 Hypothetical Protein
45	0842 (CT702)	CT702 Hypothetical Protein
	0843 (CT702)	CT702 Hypothetical Protein
	0852 (CT711)	CT711 Hypothetical Protein
	0853 (CT712)	CT712 Hypothetical Protein
	0857 (CT716)	CT716 Hypothetical Protein
50	0859 (CT718)	CT718 Hypothetical Protein
	0865 (CT724)	CT724 Hypothetical Protein
	0869 (CT728)	CT728 Hypothetical Protein
	0874 (CT733)	CT733 Hypothetical Protein
	0875 (CT734)	CT734 Hypothetical Protein
55	0884 (CT741)	CT741 Hypothetical Protein
	0887 (CT744)	CHLTR Possible Phosphoprotein
	0896 (CT753)	CT753 Hypothetical Protein

WO 00/27994

PCT/US99/26923

	0906	(CT763)	CT763 Hypothetical Protein
	0908	(CT764)	CT764 Hypothetical Protein
	0912	(CT768)	CT768 Hypothetical Protein
5	0925	(CT779)	CT779 Hypothetical Protein
	0938	(CT788)	CT788 Hypothetical Protein
	0939	(CT790)	CT790 Hypothetical Protein
	0943	(CT794)	CT794.1 Hypothetical Protein
	0945	(CT795)	CT795 Hypothetical Protein
10	0956	(CT805)	CT805 Hypothetical Protein
	0960	(CT809)	CT809 Hypothetical Protein
	0989	(CT832)	CT832 Hypothetical Protein
	0994	(CT837)	CT837 Hypothetical Protein
	0995	(CT838)	CT838 Hypothetical Protein
15	0996	(CT839)	CT839 Hypothetical Protein
	1002	(CT845)	CT845 Hypothetical Protein
	1003	(CT846)	CT846 Hypothetical Protein
	1004	(CT847)	CT847 Hypothetical Protein
	1005	(CT848)	CT848 Hypothetical Protein
20	1006	(CT849)	CT849 Hypothetical Protein
	1007	(CT849)	CT849.1 Hypothetical Protein
	1008	(CT850)	CT850 Hypothetical Protein
	1010	(CT852)	CT852 Hypothetical Protein
	1011	(CT853)	CT853 Hypothetical Protein
	1015	(CT857)	CT857 Hypothetical Protein
25	1016	(CT858)	CT858 Hypothetical Protein
	1019	(CT860)	CT860 Hypothetical Protein
	1020	(CT861)	CT861 Hypothetical Protein
	1022	(CT863)	CT863 Hypothetical Protein
30	1032	(CT373)	CT373 Hypothetical Protein
	1033	(CT372)	CT372 Hypothetical Protein
	1034	(CT371)	CT371 Hypothetical Protein
	1057	(CT356)	CT356 Hypothetical Protein
	1058	(CT355)	CT355 Hypothetical Protein
35	1061	(CT330)	CT330 Hypothetical Protein
	1073	(CT371)	CT371 Hypothetical Protein
Coding Genes Not in <i>C. trachomatis</i>			
	0486		Hypothetical Proline Permease
40	0279		Possible ABC Transporter Permease Protein
	0505		3-Methyladenine DNA Glycosylase
	0193	argR	Similarity to Arginine Repressor
	1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase
	1044	bioB	Biotin Synthase
	1042	bioD	Dethiobiotin synthetase
45	0585		Similarity to Cps IncA_2
	0562		CHLPS 43 kDa Protein Homolog_1
	0927		CHLPS 43 kDa Protein Homolog_2
	0928		CHLPS 43 kDa Protein Homolog_3
	0929		CHLPS 43 kDa Protein Homolog_4
50	1045		Conserved Hypothetical Membrane Protein
	0251		Conserved Hypothetical Protein
	0278		Conserved Outer Membrane Lipoprotein Protein
	0907		CutA-like Periplasmic Divalent Cation Tolerance Protein
	0171	guaA	GMP Synthase
55	0172	guaB	Inosine 5'-Monophosphate Dehydrogenase
	0608		Uridine 5'-Monophosphate Synthase
	0735		Uridine Kinase

WO 00/27994

PCT/US99/26923

	0980	Similar to <i>Saccharomyces cerevisiae</i> 52.9KDa Protein		
	0232	Similarity to 5'-Methylthioadenosine Nucleosidase		
	1046	Tryptophan Hydroxylase		
	0477	yqeV_Bs	Conserved Hypothetical Protein	
5	0048	yqfF-Bs	Conserved Hypothetical IM Protein	
	0587	yvyD_Bs	Conserved Hypothetical Protein	
	0143	yxjG_Bs_1	Conserved Hypothetical Protein	
	0448	yxjG_Bs_2	Conserved Hypothetical Protein	
	0006	0180	0440	0977
10	0007	0181	0455	0978
	0008	0190	0456	1018
	0009	0203	0457	1023
	0010	0204	0458	1027
	0011	0205	0459	1029
15	0012	0209	0460	1040
	0028	0210	0461	1051
	0029	0211	0462	1052
	0034	0212	0463	1053
	0041	0213	0464	1054
20	0042	0214	0465	1055
	0043	0215	0472	1056
	0044	0216	0473	1064
	0045	0218	0481	1065
	0046	0220	0483	1066
25	0047	0221	0492	1070
	0049	0222	0493	1071
	0050	0223	0494	1072
	0051	0224	0498	
	0063	0225	0499	
30	0064	0226	0516	
	0066	0233	0517	
	0067	0240	0523	
	0069	0241	0524	
	0070	0242	0553	
35	0099	0243	0574	
	0124	0266	0600	
	0125	0267	0656	
	0126	0268	0664	
	0130	0277	0677	
40	0131	0283	0678	
	0132	0284	0685	
	0142	0285	0686	
	0146	0287	0724	
	0147	0352	0731	
45	0155	0353	0745	
	0156	0354	0753	
	0157	0355	0794	
	0158	0356	0795	
	0159	0357	0796	
50	0162	0358	0797	
	0163	0365	0798	
	0164	0366	0799	
	0165	0367	0829	
	0166	0368	0830	
55	0167	0371	0831	
	0168	0372	0881	
	0169	0375	0882	

**WO 00/27994****PCT/US99/26923**

5

0170	0376	0913
0173	0391	0914
0174	0398	0930
0175	0404	0944
0177	0431	0964
0178	0432	0975
0179	0439	0976



PCT/US99/26923

[illegible]

CpN\_0028 43328 42543  
No robust homolog present in Genebank/EMBL as of 11/7/98  
RMFLFHPHPVFDQSLSFLPYLKSISGIIKESKIVENYHKGQDSVITITGVSG  
SDVHALPKISKERIIKILSLILPLILKILIVLRIILFFYKRLIGLIDMOZLL  
TPQDNLSLPLPSPTLQKILHKLHKLKLTGNTNIEGCFSTKLTIDLGAPFST  
FYSNLSLPPYFHSLSVSPNISCEERALLNYHKQEGEDHAIKLVKTHQACSFFVFSK  
QKIDKAGGSLITLFFKITYPL

CPr\_0029 43839 43390  
No robust homolog present in Genbank/EMBL as of 11/7/98  
SNQERNENYTCNLFRIYKIFFAALNIRGDLGRFCYSYILLRPLKLDLSLRKQDQELL  
KKFQIKLRTTSIKSLISLRLOOLGKREATOSDILYCTSRFOYLSNFSIEDPRIPPTNAAQ  
LQITYSRSVNLKIKFYVYLSNRKTKP

CPN\_0030 43840 44529  
 lgg-O-Sialoglycoprotein Endopeptidase  
 LGGVGVSYSLFFYIKRIRKRYKYYKIIITDSGYPLFACVNDQVLEHNSLPVGPOLGIVLE  
 FLFKNSLSPGVAVALGPGNF SATRICIS AQGLAAGNVPLIGYSLEGLYLLSKDQK  
 LAMPFLGIRGGVLLVSLSPEDGLNLRGHPGAGALLSYEASPDYVANGYHYVSPNQ  
 LAFSPDQKITEVEVAPVEDIRIRVIISQMPVEYDOKLSYDPSYSCIT

CPr\_0031 44708 44884  
rs21-S21 Ribosomal Protein  
CHPSVKVRVGEFVDRLRIKKIDKIGILKAASHRFYDKPSVIGRAKSKAAAYTR

[illegible]

CPN\_0033 46129 48171  
cpdHA2B/odhA2odhB-(pyruvate) Oxoisovalerate Dihydrogenase Alpha  
& Beta Fusion  
ERSGQVQVQVYSSIRDLV/LKLVNELFAEHLKLLRSSGSGDGTQLSCAGKEAGVLAG  
SLKLPKGDMSVPPYVYDOGPPYIGLOCDLSIEFASFLARTPHNHSARQPPHYSHQKLRIC  
QSSGVVGTGLOAQAARHVAHVSADAEVYVYSGGGATSGOGEHKLNFVLAHOLPLTV  
IQNNHAILSVFFEDSGGADIALSLQCHGLAVLEVYDGGNTLSLETTSHVAVDQAQNSVP  
LKLIDLVVLSCLSEALHDPQEKYRSALKLLSHDKPPLILLEKALNVFGLSPPYIEEIKK  
EAQEVYKSCLEIAELPPFSQKSTSEHVTSLPTLIDYENSQAQKLNSTPFIQVDEIA  
SEALVEEMTRDSGVYVFGEDVADGKGVVGTQVRLNLTGPGCFRNPFSLPAEIIATIGIA  
GALVEGTHKPVVEITVGYTFNGINLQVFEASSIYVTSAGDEVNPLVIRAPGGQIOGPPY  
SSQSGEGLFCAKPGKIVRQVYVSNAAADKALKALALRNPVTLTKALYORRISFACPV  
SHDVLVPPGKAAIVTHKQVLTYSVGNPLVLSLEVAQDLSRSGTIEVTLDRVWCFDA  
VNLKSLKTKTGLRLVLTAESEFGTSGSELVATNSGQGYALDAPIRRLQGLHAPVYPERVL  
ENVKLEPHKSTIEADAKSLIF

[illegible][illegible][illegible][illegible]





PCT/US99/26923

[illegible]

PCT/US99/26923

THE FOLLOWING INFORMATION PROVIDED BY CINCINNATI/POL. ON 01/17/74  
 YHACTYXKISREFAAKIWAQOMJL:77TPTTAATLJHVVHFAITTHVOIKHIS(K  
 ETIAVFAK:PADTVATFAIERLEHJTVLJAAKIKH497JIKHKKPI4.TRY

**PCT/US99/26923**

78

**PCT/US99/26923**

[illegible]

CPN\_0133 167349 166564  
 CPMs hypothetical protein  
 NSSATNPKLLNGLFLIGCCVIGYFPHKUESIVDQNLNRLHTVTVGRVSIINTSGIKRI  
 ICINHPLASERFPYAAIEYADVRFSSILKQTLQGLIELIGANTTIPFDSNGTQ  
 NMSLVWHPKQETSTNLDIDRAPVLIRCLPLATPLVGLRANKDDIPMLSVPSLQTS  
 HTSSAKPKLSLEAPSLVLLAEESLYNLNPGDIKPLSQANKHVFSSYSPQDRL  
 NQVATGTEVIGCFNLFLPH

[illegible]

CpN\_0135 169448 169143  
groES-10kDa Chaperonin  
MSDQATTLRIKPLGDRILVQREEEATARGGIIIPDTAGKKQDRAEVLVLGTGKRTDGT  
LSPETVKKQDITLMKKYAGQREITIDDEEVVILQSSSEINAVLK

[illegible]

CPn\_0137 172263 171502  
ygpA-ACR family  
VCSNVDADLSHLETLSSKIFQDYGPNGLVGDPQTPVVKIAVAVTADLETIKQVAAR  
ADLVYHNGIFNMGHPYPTIGHKRIQOLLIEHNIQLIAYHLPDANHTPQGGHRAVALDI  
NHMDLKGFGSSLLYGLVGQSGPDIIDISFOLLDSIOYQAPLKGSLQGGPRVSAALISG  
GAYRLSSAATSOVDFITGNQDEPAHSTALESNINFLAGHTATKRVGPKSLAENLKEE  
EETSEETITANF

CPn\_0138 174094 172700  
 "hmmL-Glutamate-1-semialdehyde-2,1-aminotransferase"  
 TNSRLFLAIKQQLGNHKKTKRNSKSNQHTVFEELACQVTPQGVNSPVRKRSVGV  
 TPVTPVSSAGAGDIFLDTHNGEGLFCQGGMAHGHSHKPKVKVIAIKTKGLSVGLTSE  
 EEELFATLNLSSGLKREIKRIFVSSCTETMTVLRVLRAGIKTRSTIIKTLQGVGHGADTL  
 LGQSTTPEITDNLSTLIDTTPSPHSLISLSPYNSKTLHHVHALCPVAGIIPFCIKAN  
 VIKVYKAEFLDGLIELCKRFLKSLSDSINDEVTGFRVAFVAGQAGDILKPSDITLYGKILG  
 FLPAALAVGHRSTLDHNPAGDIFQAGTSSNPLALMATGHAAIKQSGDPTYDLISQLA  
 LPSYSFETIESRSGFPPSVLGHQGTNLFSLTTEASPTNLTGAAKLVNSDVEVQITVSEVFIG

Cpnt\_0139 174686 174093  
YQGE  
STPTNKLRLDIDKIPYARLEKGLLSLVASPDINGVFAVSIVLLCEHSLNGSFGLIUNTLG  
FEISDDIPTFERKYSNNHIRFCMGGLQANQHMLHLSCEIPEOTLEICPSVYGGDLPLF  
QELASSESGPEINLCFCYSGWAGOLEKFLSNDFLAPGNKDYVPYSEPEDLMALVLD  
LCGYAGISVTPDNLIN

CPr\_0140 175140 174673  
yqde  
PRSNQOKIFCHSLEKELLEETPLVLLNFYKLVFSCNYAGMILGTEEEKFAIYGHVSHQOA  
FOGADTEGHSPORFANDLLNFVFGFDIQLVLRVINDYKDNVFTRLFLBQKOREFLYV  
VYDARPSDSIPLALTHKIPILCVKSVFVAUVPYEE

CPN 0141 175817 175110  
HSSA-RIDGEE-S-P ISCR08A0  
PSSA-VEV.DUHLHKKCLLAHEAATQVTCGHI LGLGCSGSTAKEFIFALAIR IOTESLAVHA  
IASOHSIT/LALAKOLA/PLNPKPKFSLDLTVDGAEVDPQJLRHKKOOGA/IFREKILIAA  
AKRSI/LI/DESKLVPVPRKFPVPLEISRPFRSA/IEEIRHLG/EGEHRLOOTGOLF ITDS  
NLY/LY/IGKVEV/PNPKDLK/LK/LK/ITG/VEV/P/IEKVEVWGSNCSGLI/IKKYSV

[illegible]





**PCT/US99/26923**

[illegible][illegible]

CPn\_0178                    218052    217789  
No robust homolog present in Genbank/EMBL as of 11/7/98  
VKEYLDFLVQRNVNEDPOTKHKCTVSKFGGESIDAKTTTQOLFPIAGKTEPGNGKCLG  
PSILKGLALGILITGVNRRERENVYLD

CpN\_0179 218550 218056  
No robust homolog present in Genbank/EMBL as of 11/7/98  
PKINOTHPETRIEATSVPKNRRLRUSPHKSGRRSPSKACVANFNFTLQAGSGIIFG  
QKAILLVNDKTPHYCSIFESIGFTNEEDLEAGHNOQAAALVRKILKVVPHNFKGLIAK  
LPSLKKDRKFNSSLIFPKLSYALDLSAPHMLGGKPNLSYEKLD

CPA\_0180 218963 218355  
No robust homolog present in Genbank/EMBL as of 11/7/98  
TSLHGLLECKYKPFVIGTIVASITTPSOLLAHQREVRDAYNGQACDKPARANOILEAKKI  
CLLDVYTHHHYSVFTPCVDYHPHLFTTVPSSQNDNGLSNPLDNLVLEAWRTHHAKRL  
LAACKIRNIEVPRVGLGDLGSLISLKLKQKQFOSLTEDFVHSTHQEGRVHQHQLK  
LSTLLKIKQAVLESTQKLRSS

CP\_0181 219175 218777  
No robust homolog present in Genbank/EMBL as of 11/7/98  
VHLEFIDGGVYTFKFKPKLFYNYVSLNSHHIDPSSLKAVQALDSYFFMGQDTTVLAR  
DDISREIYCVRLYIRFWIVSISQSLSRIPWRLRILLRYCTLRGKYVNPILIKRIALL  
GLNIFSRLEKSY

CpR\_0182 220704 219334  
accC-Biotin Carboxylase  
NCIDKQVLTIANKEIGIAVRIIRACHGILGSLTAVVVSILADQELHVLLEAATCIGPQAAK  
SYLSTANSLACITGDAVWGGYGLFSENAPFASICESGLTFIPGSSISLAWGDKIA  
RFLKSLNIGLCPVPGSGIIIEDESDKILAEKIGYFPIVKAAGVGGGGRITRVKDEFF  
FVSAAARALAGAGAPVNPVYIEKIDENPHRLIOTVIGDQVWVNLGDLCTIDGKRL  
ILTEPSPILNAELRVKGVAVDLASLAEVYSGVTFVLELDRKKVYITDQNTIVQNT  
ITESTVGTIDVLDKIDIVHAGKRLPKWQNIIEFSQNIICLNLAEDPTNPFSPGSLGLY  
LPAPGSTRVGGACSGVATPPYDSSVAGLVIAGKIDGAEZEAIDQALKEPHHGGVOST  
IEFHQPIVDFXELSLVYNTITDLAAGSFTKEY

CPA\_0183 221207 220695  
accB-Biotin Carboxyl Carrier Protein  
RLRLGDLQQLTGLMIAMGRNKHQRAIFIKREGLELELERDTREGNRQELVFPYDSRLPSGFS  
QERPITPDPIKQDTIKETTITNSETSTTKSSGFISSPLVGTGYGSPAPDPSFVFKPGDIV  
SETTVTLVEAMGVNNEVKAQSGSRVLVLTITNGDPVQFGSKLERIAKDS

CPN\_0184 221814 221221  
afp-Elongation Factor P  
QWIKIKPCCCEKXHWLSLSGVGFSTIKGLYKVTSVSKVAGPGESEFKVLAQAQSD  
VNIIDRFKATQEVKEAFETRTLELYLEDESYLFLOLQNYKLPFPOEIKHKNFLPKA  
GVTSAMVYNNVSVFVLPFLFLMVKSDTFPGDSLSSGGVKALLETGIEWVPPFVE  
IGDVNIDTRTCYTORP-

CPN\_0185 222457 221765  
rpe/araD-Ribulose-P Epimerase  
AEVKKQESVLPSGNGADITCLGVEAKKLEAGSDFIHIDIMDGHFVFNLTFCFGTIAA  
INRSTDLFLVHAMITYNPFIEISFVRSCADRIIVHFEASEDIKELLSYIKKCGVOAGLA  
FSPOTSIEFLPSFLPFCADVVILMSVYPCGTGSLPNTIEKIFAFARMAKITGLGKDSLI  
FVDTGIDDOASPLCRDAGDITLVTASYLFEADSIAMEDIKILLRGENVYVK

CPRL0186 222878 224068  
 "stabilizer to Cps Inc  
 P K D K L I A G S P W A N T P S A I P P T P T I P K P S S I E K V I I V A R Y L F A I A A T S  
 P G I K L I L L S G A L T P G I C I A L L V I F F W S W L G L I L K S I E K V A L R E E V S R P T E M Q R  
 L T V I T T I E T V K D K A K D O L L T E S K F V R N E D N I K T A A D L E D V S K L Y K S L E A L E R I  
 N O I O A N N A G A O E I S S E L K K I G M E A P W E D N I T S J A L L L K D D V A D E A O T W Y K A N O  
 I Q T O A L Q A E I L G M N N S T K S Y E N L V D O A L T R V V G E L E N L K I S O A C S A L R O E T E  
 K L A Q H E T S L O O R I D A N K A D E N L A D V T A L E K K U R A E G S E F I A C V R D T F O R E T E

CPn\_0187 224218 225045  
predicted methylase  
VFLVLTPTLTLMHSKPLSRKKNNESKEETQWDIASSYRKIVDDKHGYHIRETLITPLLP  
LITLGGSSVLDIGCCOTFLPALPCKRYALDIDLEPLFALAYARKVGNCHQVQADLS  
KRLTFVSPVFLSHAVILGSLNMGKPLAKINTATLPLPFFVLVNIHFRIPIRASHW  
VNIINDEKILSRHIDRYLSFMKPIINAINQKQDCTITFLIPLFLFWKELSGKFLVGL  
DEETCKTQTSKRAKNAKPEPLPLIKKIK

[illegible]

**PCT/US99/26923**

570 9124

570 9124

[illegible]

CPD 0199 241018 241981

[illegible]

CPN 0200 241996 242868

CPN\_0200 241996 242868  
 OOPC-Oligopeptide Permease  
 EDDKGLKGLSSAPSRSTKSTKIQNQLVGLGTTTLLKGLGALLFWFYQVETSLKID  
 LLYSPSCFFPFGDTLGRQFATKRLGRLLSLIATLIDVCGGLMVAIVASQKQIK  
 DFLQRTTEILLFLSPRIPIILLVFIHQGLPLILANTITGWPISIRIITQOFLLLQK  
 PFLSKAKHMASTFIHQGLPLITLPIALSTLIFTIPNATYTFATISFLGLTQPPAS  
 LTLTKRTINATIDVYVFLFPFSLDIALSISPLNGCATKCLGEGSG

CPA 0201 242810 243715

CPN\_0202 243682 244500

CPn\_0202 243682 244500  
 oppF-Oligopeptide translocase ATPase  
 VPTSEYARAFMTTLLSLKSLDITLIRGKILNHNMLNLNGNSLYLTIVGPGGSGKSLT  
 IDKLLPTTGTITTTMDPTPKARARVWQWDDISLNGPSYNGIKIISPLNIIOTYVKA  
 RDKETIKYDILVNPQKSVLLKPKPLSGGQGRALAKALVSKPELLICDEPLSLDTL  
 NQSLILDLFOTIKGYSTVLTITMNSAAVYIADTIAVNGQGLVTHACRCKFTFWN  
 TITGGLDLPPIFLSLISTDEKSEYLAQVASK

CEn\_0204 245691 246002

CPN\_0204 245691 246002  
No robust homolog present in GenBank/EMBL as of 11/7/98  
PRIDMAYFFRKYQSKDPFSSARSIWANPFQTHHEGNIKIKGNGYQIFTRLJGLGISTSS  
VISTNPNPFFDEGCFVWESQFSLADHGILKOKETFFYRNT

CPn\_0205                    246073    246327  
No robust homolog present in Genebank/EMBL as of 11/7/98  
IEDSKGVGSASAFRNPPOLLKFLVCEELCLTVATHRALLETPLALSPFKELKTVY  
VRADKILQHLNPNQGFITLSPICPS

CPD 0206 246346 247161

CT203 hypothetical protein  
 IVDRRSPACYDS INSDAGVSLNDISHILEDLAYDEGILPREAIEAAIVKQNDITPYLL  
 HILMDATQVPEIVNDGSGYGHLYANYLLAOFRESRALPLIKLFAFEDDTPHALAGDVL  
 TEDLPRIILASVNCNDSLIKELIETPKINFPYKAAAIISGLVTLVCAGKIPDRKIVRYFAEL  
 LNYLREKQSPFAWNLGAGICTLYPGELFYPISKAFDGLVDTSFISHEVDENIIEETV  
 ESCINTLCSSLELINDLEEDKMDLEDFPIEP

CPA 0207 247209 248617

CPA 0208 249735 250602

1991-0209 201969 2437







PCT/US99/26923

82061  
CUBA  
TO DIRECT HOMES IN CUBA/EMU. as of 11/7/98  
KUNLFFFTANKETTAHILYPPVPSFZPTUJLAJVLJJLVVVAAWATP.



**WO 00/27994**

**PCT/US99/26923**

100-443887-1000

CPN\_0306 145116 146431  
pGNC-Dihydrodipolipamide Acetyltransferase  
GKPVITLKKLKKPLSPNEVYVTHNNGSDVSGDVEIISTORALIDHTANEDQWR  
ILIRKHEKDEIVGTIPVLTANEPENLELLPTPEPNSLSPGSSSEYSPATTPA  
AGATPVTAVTFPEPPLSPGVPLVFKVGTGTLPLARLAKEDNIVSGDSSGPGQIVK  
PLSTNNGNKKVQVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLV  
PLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLV  
PLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLVPLV  
VALPDGIIPTPIICARDKRNKLISAEIKSLKALRGLSDQTEKSGVSNLQHTG  
EFTATVNPQQAALVAGSVTEQALVLDGTTIGSTCNELTSDVRVIGDTPAAMPKRLQ  
KILEAPAVLLN

[illegible]

CPn\_0308 349213 349596  
No robust homolog present in Genebank/EMBL as of 11/7/98  
FFTQEDMATVAQTPTOTPOPPSVSHKATHRYCSWFFKPIVLVSLGILLASLTITGLVIA  
SGVTLISLGTGIVLAIQIVLAGIALVLPNNITRQFQARTAELENDKIKISAPAAATVQKQK  
LEDYSSK

[illegible]

CTR\_0310 353472 351049  
 60DA-60kDa Inner Membrane Protein  
 YFTLLSLFVYQWIKRTLLFYSLIGLAFVQKFLFFQYNGVPSFCSNLAQKRIKSEDTLA  
 EAVSVGLSVFSDVDIVGEDHDSYIAVRGDKLLFINGEAAQSVYSSGESWSPVDHRGK  
 PDNIDLLILYRQGGSSFNPTNGKVLFTNHEGLPLVVFVFRNEPLVTFVYAGRIISN  
 KSDTIFGTALVYFRSGSDYITPLGLYDSKEDGLVSLDPLTRAVITFGWDSAKSSDANTH  
 LPLVDNDMYITLSEESGSIETGLINDPSTNNKSNVIEIGFDLASEKSPALFPGLLSK  
 LPPGQAGNSISGQITPLLRGLLSDSKILLPLEYHALVNVGRLATPVALRYLVSYTP  
 NISQLESIDRSVQKVKLPLPNDPQVVFYETATLTLTEDSYVTSQVPEINISNAP  
 IRTYRVIDNGKSSDKVLKPKVEPLARGVYVITKESNGCYFTLLPSELAQYGS  
 YVYSGSATPTPLRSAPNQLYVPSKYGVETVLLPLPDQATHRFLVYAGLPAEPTLVKL  
 LQDITLQEDGENPEYLSISPGRVAFVETPAALLFTIDKFFPLVTGSMGSIITLLVPL  
 LGLPLVLAHSIRSDHQLISPTQIQOQYKNEPRAGHIEGLYKTNKTVYPTOCLE  
 LTLTLPPLIANDLTKSSTFLGSAFIPGWINDLTPADVFLSWGTSVITFNIEPFLPL  
 GLVAFVLOQYVTLKHGQVLPDQOQOQWGRHQAAILFTAMPYVFPCLNIYVLSMHLI  
 VQQMTNKLISLKHGLGVVANNQDR

PR\_0111 354453 353575  
 TC131 hypohydrated protein  
 MRADNAYVTVWDSKISVWFERNSLALTWGVVFTVVGIFLACLARSYLALSYVQLKDLHS  
 SSKSOLVALEDFIYISFLITVGRALYAVIPYGHVSFTQHPKEIIQIWGGSSKHGGVL  
 FLFLMAAIFSWHYKKISKRLFTVTLDCGSGVYIAAFTIRLNGNGLVAVETVGTPLSPGV  
 VSDPQGVKSGGVVPMVPLQVYGISVAVSGSILYFLYSIKRYLNLKGVVTSIACISVAFI  
 FTADYVSKHGCKVLAEDCLTGIGLSIFLPLFGVALLTCSLKARRHSMI

Pn\_0312 354518 354976  
 T101 hypothetical protein  
 TARNIKYKILILPFGILWISAGKLLIKATAIALDPLSFFTYCLLSNVSWGLASLKHR  
 LLSKTIRKQLSLSEFFSKITWYAIYKQTFISRRFLIMVIMIAFSLVLRRIYSNPOAL  
 VIRATVGYALIKTAIAYPSKLQNALNENPEGN

PH011 354957 355355  
 KPS-Acyl-carrier Protein Synthase  
 KLLKEISANSMEIHHGTDTIEISIREIATGNNRLNRIPTAECKYCLEKTDPIPS  
 AGRFAGKEAVAKALGTGICSVVAKDIEVFKVSHGPEVLLPSHYAKIGISKVILSISH  
 KEYATATAIALA

PKX\_0314 J56285 J55353  
 rkb-Thioredoxin Reductase  
 IHSRLT IIGSPFSSQVLTIAASRLLIPLGEGFSG IQQGGLMTTTEVDVPGFPEG I  
 GPGLKLNKKKEDQAVRPTKTLTGALL IIVSPDSYRFF ILSKSKETYSQAC I IATGASAKRL  
 IICATGAEAFQKQACACVCDASG IIPKQKLV IYQGGALSAELALYTRVYGVAVV I  
 RDRRLIAAFMKAEAKAGAKK IITFLARGE IIVKLSQ IYRSDY IKNVYQET IITTRAEAVV I  
 AIGKQVDFPLDGLTLDSEY IIVTEITSTKTSVYVFAAGVADKRYIQAIVTSGSCG  
 IADWDFPLG

156777 156716  
 EL 31 Ribosomal Protein  
 LKPKLQKCKKLNLELDELVAEFLVLYTAHPITLSEEEENDEKFFAILKLVTV  
 INKDPVVMVWLLKLRVLPINTEFLDGGSLVLAETVEVYLQANDNEKFFVLRKRAKTR  
 LKAPYHIAKLSLSLVQVQITRKEKSLVDVKEAFPLQSLINKKLLKGLYQKVC  
 PKLKLINPKRNIVVRELLKELAFKSKKELLFLTCGYRAVNVNITPFFVFLD  
 LDELIIITLTKNKLINIKKELKELVLELTKAEKFRVALLKQKRIHMDIEK

KYPTGKRVLCXIVKLLPYC (EEG)EGIIHISDHSWYONIVDPFEYAKGDEVEATV  
LSIQKDEGKISLGLKOTERHPWONIKERYPIGLHKNIEIKGLTHYCAFELEGPICELIH  
ISDHSNITKCVSHRELEKAGNSVAVLQVXESKEITFVCLQACGMBRELEBAPRAGT  
VLSGVVTKTAFAGFVTELOGILEGIRVSELSKPPAKTETITISIGENBARKDELPON  
KRVSLSVKEYLADNAYDQDSRTELDPKDSQPKERUKKCK

[illegible][illegible]

Pr\_0318 362704 363126  
b1A-Ribosome Binding Factor A  
MSYNNHQSIIKHNNLYKCHTNRRIKRVNALLQEAIAKVLKDKVHPKISNLTVT  
VSLSTDLHSARVYVSVPNPHETKEALALAKVSAGFIARASIONVLTPTFLAPYLDG  
FSPQYIENLHQIQEKES

Pn\_0319 363133 363879  
 rna-tRNA Pseudouridine Synthase  
 ITTGNLNTIKDNTDLAVELKEIGILLVPGKGRSTFSLIRALTKLGVKIKAGHTLDP  
 ATGVVWMLIGRAFTLDELPEKYEALAKGLTSTVSDYCDGGRVGRSKISLIEV  
 SAARYQYKIGQLPWRSAKVQKGLLEYARGLSIEKRWSTVQVHGLTKYETFLM  
 VVSCSTGYTIRISAKELGTMLCCGAYLEQLRLRLRSGRFSDEICTDGLNHPDPLSY  
 RDAHGSL

FLB-020 Synthesase

[illegible][illegible][illegible]

124 hypochlorite protein

**PCT/US99/26923**

CPH033  
 IEEIFPGNOGRKLLIVLRMNCFLVGLSPINGEDLMAOKEVYSIRKALRNTWATL  
 EAGIVLTJTEIKSTRDNGOGLGDAYVPSGEGCQNGQFIAPYKEGIDYRTEEDKGLL  
 LHYRELRLKLEKLAQKNTLIPGLNLSRGYVYKRLCCRGKAYDKRRITITREKLELV  
 AAKNRKHH

[illegible]

CT339 hypothetical protein  
VTTLPHQPKICKSLKLNFRHISDELSLAPKLNLYAOGKTNLLEALVYLSLGRFTRKQLT  
DTITFGSSNFFLETQFQKHLQALSLSYTKGKIKICYNQLPINTLSOLIGKVFVYLPSS  
KDRLLISQAPADRLFLWLLSQDNNHYTCLSYNRLQQRNALLKSKQTSVAGQNS  
WNTAPATVYNGFSVVRNQLYPIKNGLT

PLYPLLVLSRSSBAKCSLKQKQANLRCUWDEQLVHGTYL S IORFLCSQKLSOLSKEL  
WBAK KEDIALKFKSLKNSDISETAVAEETHKOLSISLPRDL

CPL\_0341            J84160     J84495  
(frame-shift with 0340)  
GTSVGP~~H~~R~~E~~D~~F~~L~~T~~I~~N~~G~~M~~PVSQFSSEGGKHSLLA!LRLAECTLYLKQSHNVSPLVCLDDI  
HAGT~~E~~~~R~~~~R~~~~E~~~~V~~~~A~~~~L~~~~L~~~~I~~~~D~~~~P~~~~A~~~~P~~~~T~~~~L~~~~G~~~~O~~~~T~~~~I~~~~T~~~~S~~~~T~~~~R~~~~O~~~~G~~~~E~~~~L~~~~P~~~~K~~~~T~~~~S~~~~I~~~~V~~~~I~~~~S~~~~I~~~~E~~~~N~~~~A~~~~O~~~~V~~~~S~~~~D~~~~O~~~~I~~

CPN\_0342 384619 385062  
predicted OMP (leader (19) peptide)  
HNGQFLTLTFLAVGNPLFSETSVIQTLPSCIGGLKETSKOKESVVCVNAFLRYSYELRP  
IARVLEKHEIVDFVNNYETKRFLEKHAHLNRLIAKIAELKPGVFINFVTHSGQGVTR  
VALNPDCPEKAKCKEFLNLLRTOGLH

CPM 0363 304999 303999  
(frame-shift with 034277)  
LPRRSOKKAILNAPPNAGSTLARRYRCVKFVQVFGGKLGROLLTYCTPQELANGKLP  
SLDVLILSGNRSTFLPRLPYENDGKCTIETKLDTPKAYVVIHTSHYIITNGBLYL  
KCEFLKEGNTTPIIENVPEALEQTVMEDKONSLKPYPNODIYVINCFSRPNLYLQ  
FQMSLRNORNEINPELKE

[illegible]

CR1R3L  
 CR1R3L hypothetical protein  
 LKACVLAELVAGLSTGSGIGRITLTVRRYSPSEFKIISAGYGNLRLFPQOLEEAPALAA  
 AYLALNVEYNACORPPIHPTVQOGLLTQIDIMDTVTVVAASGIEALPAITLSSGKQK  
 ALANLANKELVAGELVSKTKAKNGIKVLPIPSRBNALYCGEETIKGILITLSSGQ  
 PLLAKSLLEELSCVTQDVLNHPITWNGSKVTVDSTLVNKGELITEAYVLPKQDNLVLA  
 VTPHOSLNGPPIVLCGVSITINHPDPIPTQPIQYALTAFERFASPDAGNDHSPGKGLFT  
 VPEERFSPISLAVGQVLEKQSGSFPNAANEVLVRRFLCEEISWCDILUULTTUMCNK  
 VYVACHSI-FDI-ILVQDGAARLAAEII

[illegible]

CPD0347 131018 389674 Protein  
 049-050/YGEC-I-GLGSH-Hemoglobin  
 TPTNPEALSRKLTIVILMLISLDTLTLSFSLAVLTICHTTALMTGLTISLQNPFLLS  
 ELSLSHASVPGLLGLGLASVYSLQAGIFWVLFGCAASVTFGVIITVPLKGLKWDSDA  
 KGLVWVFATIGVLIASVKESSPTLRINAYLGLGKGLFLATLAAIVTCASLAL  
 NAYRQIVYIVTDPKDFATVCTLKITLYEALSLITLIVSLVSVGVSRVSVGLISANFVAPSL  
 CARGLDRSLRTILSLSAFQITLISGALGYSIVAPTKRATIGQOAVPTVLTPTGLPWVAC  
 GGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV  
 DVTGPK  
 GLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV

06R-cr38/yt08-ADC transporect ATPase:  
 LITGLAVYDPTTFPIKVNKLVYDHAAYIIYIIIFGKGLSLTAIIIPNKGKGTLLKASG  
 ILYPSGDTTFPIFNQKAKTRQPIATYAPVYIIIFLPHPTTVI.DLALMAYSYKIMKRGIS  
 QDQPREAFIILSRVGLSYAGROIGOLLYAYDQYAFALAHAKKQADLYLDELPI:ATDAS  
 PYSYVSYLQELRDOGKTIVSYVHDLCHIVROLFTAHVLLNKLRIICGPTPDE:LAUDIPOT  
 IYIIELEGLKLLDNLKQYKQ:

997-1729-0000

**PCT/US99/26923**







**PCT/US99/26923**

[illegible]



**PCT/US99/26923**

21

[illegible]

WO 00/27994

PCT/US99/26923

YFVQAAALHRTDHTTGLSPZYLYKTNAPF LSEDTLLSFFQDFPVYTKSEA  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0455 520363 519458  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0456 521568 520327  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0457 523886 522120  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0458 526344 524236  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0459 527062 526619  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0460 527840 526992  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0461 528647 527844  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0462 531124 529037  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
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 DQKQPTNHRVTLKLT

Cpn\_0463 532480 531971  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0464 533278 532971  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0465 533718 536537  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0466 536528 539434  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0467 539608 540432  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0468 540399 541660  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0469 541357 542532  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0470 542561 545401  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0471 545401 545401  
 No robust homolog present in Genbank/EMBL as of 11/7/98  
 LKRAATYVTHHNTTYLRDPAKPKDQZNNNSYVLIADNPFLMCLLTPPLAQA  
 WDLXIFIAEPFLOQDQPTTETDLOQDPSKGRYVNSLPICGSSOWPTPKAPASTLT  
 KLAYKPDLYRVNPHNITVVGQESTSICANLHRLGLFVQINDVOLTEDTOALNTY  
 DQKQPTNHRVTLKLT

Cpn\_0472 545401 545401



**PCT/US99/26923**

96



**PCT/US99/26923**

24

CT19H hypothetical protein  
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 KQAGGELTVLSKEELASTENSSVTEKEIFESIKKINECKALLKQTELOJQATPFL  
 SIYERLLNKKRQVWPVIRVQVSOCHIVLTPOHNLVRKQKALIFEDCSRLYNQESQ  
 UNAGINLAKIKRRRRRAAV

526  
VFNHLEKSPWCTUJLHLEKXENHJSTNLTUCCDHLNKLKAGVFFTOFPOKHEAN  
QLEKHLGHSSGJFTSVGVGKQVARKVLTQSLSERALFTSPVLLUNGGLGVSPGDI  
VLFTSKSGDTEGLDITVPHLKSRRAILVITGNMPSYBLSAALSDLVILSPVLSFV  
ITNTHYVGNGLQGLAMLHPSKSGVLSYTGNGHSGQKANGKGVDFNPFKTEVFFC  
HLEKSPVLELVSTAGCCCTCTVPOFVPLNGITFCDGLRSLASGYGCVLSLEDMVT  
USBCITFSDIATLALQDSSSPFVPLVPLNEDENRNVLTLLHPTFLAKGLL

CPN\_0527 609910 608726  
sucC Dihydrolipoamide Succinyltransferase  
RYNKEFPAFQKIGETSSGKIVNQLGDNVADREPLVSTDXIATPLSPAGVLR  
FVNCNEDVAFQGVGLITLLEISLADDEESTCSPTCECTKAGSSSSVAFSVLR  
AQREGILDLNQLKQITKGRVIRDTOLREAYLSSEQVSIPEITFGQGNILIPSLRA  
ASLSKSDSEPHASLVNVVDVDTNLNLSIGTRGVRLDTNCHVLTITSTIVQCLAKRQ  
FPLNGLSDGTITVNRKGVNMGVAVNLRKAGGVVTVNCGDRLGSLAKALALSSAR  
LNLKLESEVQGGVSTVNTDGTALGKPTVPEVAILGICQKRVNRDQSLAKR  
LNLKLESEVQGGVSTVNTDGTALGKPTVPEVAILGICQKRVNRDQSLAKR

CPR\_0528 611165 609921  
 gct-*Glutamate Symport*  
 LKQKAKIKFIFGLFVQVLTGLVLEDAIKFFPKIDIFNLNLSVYVPLVFCSSVLGIVASIS  
 DDQGLGRIKIGFVLTGLTGLAIVLGLCAPIHIFSPNGGCFDAQAQSDQASVIVDIBRT  
 AAYFLSILAAQVTFSPNPRFAGNLIQIIIFIAITGLIALSLGDRGPRVQIDQFSEIN  
 LRVKMTKISFATPGQAGSMATVSNHGLGVLQKQGLIAYLCAICPLATVPGVGLV  
 CQKSFSLSPGDAALCAVSAFASATATVGLVGLVGLVGLVGLVGLVGLVGLVGLV  
 GTALPGVAFVIAQVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV  
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[illegible]

CPN\_0530 613323 612460  
 spoU-rRNA Methylase  
 SVYLAKGFLARRGSGLAIFKFCSDICIGKHNPVKEALALKRSRKRSSWFLVDEAREIQ  
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 QIATVNGKDFLQRUNQAOPPLVITL EVDKPGNGALIALADGAQGVDTVLGKTVNG  
 NVRRSLGGLAVFLSLPILSISREHGKFLKDGEGTVFTVS PRAETHYTSIKYGLPTALVKS  
 FETGLTQWDSDFSEIALPGHGSDDSLNLAIVAAVAYEVWRQWNV

CPA\_0531 614198 613245  
SAM dependant methyltransferase  
PSKKQFKXIKGRKRSYGRDVRVNNKTRGKSHKFTSLIIERLVMDVYKLLDSCGQKCLCK  
GFTLLRPSSIAVWPKNRPSSQAQQLVREDEGRAGWPKFLPMEHVAFSDVRLCK  
FTFPGHGLVTPGPGKALQKIKKHORVNLNLAFTYTCAGSIFAAKGGVFLVMDVDSQ  
AAVRGAQRVNEVQAPNRPFRFVMDIVSFLKKEIRNNKUYQVILLDDPYGKPGGVV  
TKDKDLFPLLSLGSLKADASYFLLTSHTFGHTPEFLRAAIRASVPTLVSEAMSCGSF  
CGEGVGLPSCGFSVQWIA

CPrn\_0532 614716 614075  
ribC/risA-Riboflavin Synthase  
ESPCKDSDSVVKHOGVSGIIQELGEVCFEAGNGLSLGIKSTPLFVPLVLTGDSVAVDG  
VCLTSLSNESKIFVDFVETLACTTGLGEKRCSDVNLLEALHOGDSIGHHLSGVVGT  
AEFLIKENRYFRGSLKEISYLFKFGFIADIGISLTLVSVDSSTVFGFETLQKRTLL  
GKRGKFRVNIETDMSIKQVDVTFRIKLLASGKD

CPN\_0533 614910 615305  
CT406 hypothetical protein  
EVAPHQPCFNMHGELKVIDSRNAPENAIKRRRECLKCSQRFPTTFETVELTLOVLKRDGR  
YENFOESKLINGLNAASSHTRIGODOVHAIASNVKSELLGCKNREISTKEIGELVWRYLK  
KADMIAYIRFACVYRRFKDGLGELMEVLLSATPDMEK

CPrn\_0534 615389 615784  
dksA-DnaK Suppressor  
LNTFRSKVPLSDDEIEDFKKRLLEKAKLSHTLEGNAQEVKKPNEATGYSQHQAQDQTD  
TFDRTISLEVTTKEYELLRLQINRALEKINESSYICDVSCEEIPLARLIAIPYATHTVKA  
QDFEFKGLLGGN

CPn\_0535 615763 616296  
LcpA-Lipoprotein Signal Peptidase  
KRTPTWLKLSMAHPRSTLLVLTLPVLIDWTKLWLLQYKDLQILTIPTLYTHSMGRFS  
FSIAPVNEGAAGCLGFLSNVYKFLPLRFIVLIGLLAYLFKKKSGTSTQTALVLCAGA  
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CPn\_0536 616300 617621

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N11P021UKY:EWAL1KFRKLDROD7V000PH7FL1KAFKTPV05VALL311YUVE1
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771VKVPH1FLHLL1WNL6P0YK00GAL07007VATV1H0G1SRAAY:3311G0P01
100E22KAPDP7VWAL11UG11DNL1TTL1LHVLAL1TGL0W1LGN00V01L1AYF
100KFF1177V0V07TTL1:5YFL1P0P0KFL1G0T0GK1YTL0W11L1H1P0Y0NT
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Сред. 01.17 01.74 01.182

**PCT/US99/26923**

[illegible]





PCT/US99/26923

07-05-80                  679516  
57471 immunological protein

PCT/US99/26923

[illegible]

PCT/US99/26923

[illegible]

**PCT/US99/26923**

[illegible]

**PCT/US99/26923**

104





**PCT/US99/26923**

106



**PCT/US99/26923**

Year	84.000	84.005	84.010
1970	100.000	100.000	100.000
1971	100.000	100.000	100.000
1972	100.000	100.000	100.000
1973	100.000	100.000	100.000
1974	100.000	100.000	100.000
1975	100.000	100.000	100.000
1976	100.000	100.000	100.000
1977	100.000	100.000	100.000
1978	100.000	100.000	100.000
1979	100.000	100.000	100.000
1980	100.000	100.000	100.000
1981	100.000	100.000	100.000
1982	100.000	100.000	100.000
1983	100.000	100.000	100.000
1984	100.000	100.000	100.000
1985	100.000	100.000	100.000
1986	100.000	100.000	100.000
1987	100.000	100.000	100.000
1988	100.000	100.000	100.000
1989	100.000	100.000	100.000
1990	100.000	100.000	100.000
1991	100.000	100.000	100.000
1992	100.000	100.000	100.000
1993	100.000	100.000	100.000
1994	100.000	100.000	100.000
1995	100.000	100.000	100.000
1996	100.000	100.000	100.000
1997	100.000	100.000	100.000
1998	100.000	100.000	100.000
1999	100.000	100.000	100.000
2000	100.000	100.000	100.000
2001	100.000	100.000	100.000
2002	100.000	100.000	100.000
2003	100.000	100.000	100.000
2004	100.000	100.000	100.000
2005	100.000	100.000	100.000
2006	100.000	100.000	100.000
2007	100.000	100.000	100.000
2008	100.000	100.000	100.000
2009	100.000	100.000	100.000
2010	100.000	100.000	100.000
2011	100.000	100.000	100.000
2012	100.000	100.000	100.000
2013	100.000	100.000	100.000
2014	100.000	100.000	100.000
2015	100.000	100.000	100.000
2016	100.000	100.000	100.000
2017	100.000	100.000	100.000
2018	100.000	100.000	100.000
2019	100.000	100.000	100.000
2020	100.000	100.000	100.000
2021	100.000	100.000	100.000
2022	100.000	100.000	100.000
2023	100.000	100.000	100.000
2024	100.000	100.000	100.000
2025	100.000	100.000	100.000
2026	100.000	100.000	100.000
2027	100.000	100.000	100.000
2028	100.000	100.000	100.000
2029	100.000	100.000	100.000
2030	100.000	100.000	100.000
2031	100.000	100.000	100.000
2032	100.000	100.000	100.000
2033	100.000	100.000	100.000
2034	100.000	100.000	100.000
2035	100.000	100.000	100.000
2036	100.000	100.000	100.000
2037	100.000	100.000	100.000
2038	100.000	100.000	100.000
2039	100.000	100.000	100.000
2040	100.000	100.000	100.000
2041	100.000	100.000	100.000

[illegible]

**WO 00/27994**

**PCT/US99/26923**

Q7N0741 457414 958375  
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 RRLCNPLGALVHNSDPAVLGVYIIPVGVCEIRGLKEKTYGSARGAYPTVHQEADIKAS  
 REENKILDTLHRENGPAAVLCGGDEVLDTANLFLSSFLNSTEPCSK

ELLYYSFSEKONYGUMNETKRSTIYNLPDRUKALEAAVAYIEKQFAGSINSLGRHS  
 DETHSTIKTGALESGALDTHGVPRVRIIEFPPSSGKTLATHIVANAGKGVVAY  
 [A]E[AL]D[AL]PSY[AL]L[AL]GVNI[AL]DL[AL]H[AL]PP[AL]G[AL]D[AL]E[AL]AL[AL]L[AL]S[AL]G[AL]A[AL]V[AL]I[AL]V[AL]I[AL]S[AL]V[AL]A[AL]L[AL]V[AL]  
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CPn\_0763 860520 859972  
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 YLC

CPrn\_0764 861819 860524  
 C7648 hypothetical protein  
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 YKVDPLAPQYQKRVKVRQKRGDVAITHTNGIKQYKLECLNARAYGRYRWKYN  
 GNIIKIQAYVGGIADLHPASAEKLFQFTTAYNIDGIELAIVYKGLKGGVSVYHTN  
 QNTKWCPEYHVGKPGKFLVYTSKGLLKQDQYQKGRGLSTVYSDSEEDQWLAEVHT  
 EGRLLKAGYLDPOTHEIYVATHTNGIQIAYGYKVAIVETRAFGPEYGRKVTFRDNGSO  
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 KIPYQDGPGLN

CPN\_0765 862415 861801  
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DHEDVTYKHVARISKDRNTLSIESLNASCQRLPLSKERLRAGCSNLSLAQSKIEWR  
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Cp\_n\_0766 863785 862394  
C7646 hypothetical protein  
SQQGDIIVPHVIGLTIAWENTIKIALQIKQKQIVNCHCEQDIPBGTHTWSLPKGYFAAFTPT  
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SLLIQYALMATWVLSGLVFLKLSLSSAHHGAFAPCFEYVPSLSAAAKKATVIAKLG  
KQSAHNSPLLPFTPTSDTQFLFLAKHSSSELSIKFSYFTPTDTSYSPKSNPLPSYALVE  
VQGGQEDDIPQFLKLSHPLQVNSLEDSQRTSKQFTLSS

CPN\_0767 863878 864177  
CT645 hypothetical protein  
NIMLSYLLRTAINVSYFLILAYIFASWPDQSQARWYQLVSKCVDPLNFFRRFVPRIGF  
IDPSPFVGLICGLILPFVILVRLVRLFIILNPHSPMLLOYL

CPN\_0768 864144 865163  
yohI/nir3-predicted oxidoreductase  
YVFSTSKAAIPITINIIILRSSYVAPLGLSPDYPRCHSALYORGLNFCIMWKEGILVAP  
YVYKGLKLYDNNRNRIQAGLQSGNPPTSGEAAKILGLGLFDLDLNCQPTDKITKDSG  
KSLCTLPETLGRILKLTINSVSIPTVTKIRSGWDDINVEYTRTIRDAGASAVPVNIR  
TRACGGYHPSKQSYISRAKAAAGKPPVFGNGDIFPEAAAGMLTGCCDGVLVARGTGLA  
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APWVIRLSSGLAKTSYQYVCLNDNIFPADSSLETIVK

CPA\_0769 967763 965121  
 CP2A DNA Topoisomerase I-Fused to SWI Domain  
 ISIGQPIA IRLKKSLII IYESPAKIKTQLGCSFVFASSIGHIVQLPAKEFGIDVQDF  
 EPYQVLPQDQEV IINHKIRLAKCEKXVLPSPDIREGATIANIQLPDSPLIQVSVFN  
 ITKNAVTEALKHPIT IDHALVNLQQAQRRLRIDVGYKIVPSILRSKLQSGSISAGRVGS  
 VAIKLVLDREKAI IAVPYVEYNLNLVQDQPKTTFMWLVAVOGKKVEKIEPEKTN  
 IVDL INSEERAKHYAEELLESKSYITRVEAKAKRRFPAFPTTISLQSESRHFRFSAR  
 IHTS IAGTQYGEVLDSDESLGTLITHTQDSVVPDEALTITVEY IQOTFGKVLPEKANV  
 ITTKHTQDQAEI IRTDNLITPKLQNLSDQFQVYNLWKRFVSAITPAIYQTVLAV  
 ITTDTTEIDLRASGLSKPKGFLVAVYEXQDDNDQDEEHPPLPHQAQDALIKVEESVQD  
 IGLPLPRFTFESLVKELESQSGIRPSTYITINKIQESITENQRIJRLPTELGTIKISO  
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 INHIFISYQSEPCVTSINSIDAVITKSYGTEKIPYKNTKPEKPKSSIKTAAKTPSKK  
 ICKSSSVKVSSEKQITDPLFLSPDLAKINQVPSRDSAEATTKINDYIKEHQLQAPENKIL  
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Fm\_0770 868122 869131  
 T742 hypothetical protein  
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 VLIHIAEIVAVRRKRIEPEVEEVLAYOTSRWRRFPPLPRSPGESVLLFTVLGLGIL  
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[illegible]

NLRKREOTLLOVNETLLPKC JCKIPAPYPLG:KELACDHFUETT:FRATENKAVA  
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RTVAKYNAOLKILPAMPRPFPY:KCHSHRFRDCH

[illegible]

CPn\_0773 872485 873195  
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GLCSWANGQIGILLATVTVRAGEPFSHAGKQWELFDTAIVTKLQIKTHIIIFVAGAAA  
RKCKLTPNIOGHAVLSPPSHPLAAHQGFQCSHFPSKINYLAKLKPHTNKGLP

CPN 0774 873183 873425  
CT606.1 hypothetical protein  
LEAPNREGINSVCFKTPRLTAKSVVSHENLLTTOQLPSAECHPSVANLEADFLRAEALL  
AMETKQCI FQSLATTVRF

CPrn\_0775 874040 873414  
yggV family  
ERPFKTVLIASSNGYKIRETKTFLKRLGDFDIFSLSDFPYKLPQEGDSITANALTKGIH  
AANHLGKVLQIADDTLRLVPALNGLPGPLSANFAGVGAYDKDKRIGKLLDMSLSLEIVORS  
AIFECVVLVSNGEIKFKTYGICEGYLSHQEKGSSGFGYDPFVKYQYKOTFAELSEDVQ  
NVSRRKAKGLAKHLQSLFEGDLITRD

CPN\_0776 874180 875487  
 C7603 hypothetical protein  
 FTVLQVLTGSLIAITQFSLSTPMKIIYSYKVDLSCIFPVVGCAQVFLDRIPISEGEHT  
 CQGLALISKAANISQGDALSVYSRQDQTEILCTLENGYGGATPTETVGNQPS  
 CQRLSVALSYLVGKVEKVAENHCDVYVQDVGIRSVFVTLQKIVKASERYGKLL  
 VLDRNIPMGRVTVGDLNPLTSCSLAIPYCYQDTPGELALFMQIVPAAMWVITPKG  
 HENKSTDTETGLINMPSQVLPDPSPPFYFAATLIGLVASISVIGUTLFFPVLGAPIN  
 CDEVADELNRKGLPQVFLDFPFYFPTFGKYNKHCQVLLVLQDQKIIYFVETQCTG  
 VIKLQPKQVDTGLKSTIERIPARRASSICNLFGGDEFLSTISKERYIWPVLRLLCEKSES  
 VLKLSCLLSEYAES

[illegible]

CPN\_0778 877400 878092  
 tsa/ahpC-Thio-specific Antioxidant (TSA) Peroxidase  
 AFVAGSDRVPQYEPGGRFESSLVRRNRKVEEVPHTLSLVGKGAEPDFAQAVNGEICT  
 VSLKDYLGKRVVLFYFPKDFTYVCPTELHAFQDALGEFHTGCAEIVGCSVDIATHQWL  
 LQATKGGIGEGITVPLLSDEDKVISKTHYVKKFEELSFGVFLIDKGGIIRHLVVNDLP  
 LGRSIEEELRLDALIFETPNGLKSVPMNHGEGRAMAPNEGGLQYFGTID

CPrn\_0779 878502 878095  
CT602 hypothetical protein  
RFDLIFQKQFTVALFGAENGSYDTAYFCRSLVDLHNYLGDVSSPGITLAIKTLSDYNY  
VYFRVREEDYCVDSYFGLHFLNTQTTLQNI I A IGLPGVGNQHI IEASRLCKOKNSLLL  
FSDHDLYLTLTFNPP

CPN 0780 879241 878591  
 pqpQ/amiB-N-Acetylmutamoyl-L-Ala Amidase  
 HEVTEIVYHLSERLDEODSKCKQWTAAPETLAQKIRELESOKALAKTLAVLTTSYVKDLQT  
 NQLSKLQEIQKDHRLAQLDGLRVRSLSLALVDSSEPGAYADFSDPVPENIYIVREGGSL  
 LIAKKYKLVTELLKINKLDSDAIYAGORICLLOPNKQ

CPN\_0781 879851 879199  
pal-Peritidoglycan-Associated Lipoprotein  
PALPSRRKTVPLLCFSPSTAKENTHHSILWPLCTLLALLALPACSLSPNYGWEDSCN  
TCHVTRRRKKPSSFCFVPLYTEEDFNPNTFTGEVDSKEEYGYKSSQVAARNITFATDSYT  
KIGENLAILTNLVHYNNKPKATLYTGHTDEGAASVILALGARRANA[KEHLRKQI  
GADRLSTISYCKEHLVYNNINELAWOQNRTEFFIHAR

PTL0792 881077 879771  
 rib-polysaccharide transporter  
 LRLMLKGLQVPPFFAGLVLVAAELEAVRRLEHITLPIEVKOTOTKDKIKQKYLSE  
 LTFPLQIDALADLNTAAKESSFLALGHLVLPGLTLLVLSKTKTQTLTSTLQAN  
 LNDVPLVLIHMLADDTALGALPIQGLGKLVFALSSLCYQDKLQKLEMLTWTYVLIKIALP  
 TRLTLLITTKWLVKSNFTYGLVGLVYVYVPLFLQSLDELKKVLKQKALMLTYS  
 NKKKILALVALTANMLPLQLKSLTQVQWGPRLPLNELFQFQTLQWTFNFMPLVLS  
 KKKLSPFLYLKLELLELVALRLTKKYPKSSFKAGPDVPLFAPGVKQVQLQVLLFES  
 LKELVLTGDTTKKRLTWALEDRHILVFDALNAEESLYLISLVTKTKNLAIDVKKRP  
 SVAKFQDITKRL

MMKYLIVYAITAIIIGSIIILVFAEELPKKKI/PKAFDEKLVTIQKPIVITICWVVIP

PCT/US99/26923

[illegible][illegible]

CPN\_0794 897123 898004  
No robust homolog present in Genebank/EMBL as of 11/7/98  
KS SGRSFFLLKSSQGVLSLYKWNMSLQGLGSLCYSTVAA:LFH:PSQSFADSLDLGL  
GLDPSVECLSGDGAFFSVGYTFKAGSTPVEYQPKFYDVSKITLTLVETANQSGAYGIS  
YGTGTFVGTCLSLGAKNGKNSMADGTLPLTGTCVSTLEEARL SIKGTVDIGCFSSA  
SQSKAYQWASAGTTVQLADLSGGRSSAYAYALSDGTG:VGSSTHITKRLTAVIWN  
NVTPTLGLGSDASTGLYISGGGTVTVGAANTTVLQINQESHAHYNNKMD

[illegible]

CPn\_0796 899280 901340  
No robust homolog present in GeneBank/EMBL as of 11/7/98  
SLLSSLSLTGCLPLASLPRNSLAPLCLSRSTGKVRKSRGKFKVLTTPMTYVTKDUMVAT  
LALTLGPGSTNATLVADIGEPRHAAQAGVGVGGCKTVLIGKVPDOPMTATPTVYVTDKGL  
VSDAGKVGQGNRLNIGLSSAVSVKMDKVDVTLTGLSPDVAKMKNVNGKVELNGLPTLDSVABA  
SKRTAVTAVGIDGLVTVIGTLTGSLTVASAIISTGCTVVGGSNADSOHTAAYVINGVMSD  
ITLGGTFLSYLAAVSSDGSVTVGVSTNEDIRYHAFQADQCNVDLGTGGPVSAGGVSG  
QGLVTLGRRAGVPSGDNNHFLPQCPQAPSPALPVGKSTVTVSCNPKGVMDVSTLSELIQSD  
DQQLRLIQAHSAGVSSVSGAPSTVSVGAKISKQSPAVAGKQVOTKFLSYRKSQNGVGN  
OGLTGAPFVDMKLSAASGKPKVVALHYGSDALVERAALPTDGGGLSSVSCGFGQGVG  
RYDNLGETVLPFPGKIQVLLSLSDGYSQKRVFVPSVDSYVSAATSFKHIAVFAELS  
PRDSTAAATLVGRDLNLSLDTKGSVSAAGNFVLENTSVSLRPFASLANYTVDRGQGLV  
TLVAANNQDPIITLTLSDRQSSVLSLF

CPH\_0797 901552 902694  
 No robust homolog present in Genebank/EMBL as of 11/7/98  
 LKMTWTVNVLTKLSSKSKKIKVLGHLLTCTFVGLGCAALANSIGYATVSTESPTKSI  
 EDKMTWTVTLDLLSKDSSKAVGASVGRSIFVSGAGCGQVTSYATWESHLDPKLTSL  
 GEAASAGIISDGEVGVGVGDKETKTLTAFVTDGDKMLDGLATQYVSARGVSGKII  
 LQVSTATARGEDYGVGVGDKETKIKQLKLPGMLSEANAISEDTQTVGROETIRGII  
 VAVGVNANVSLTGLGGSVASAEALISANGKIVGHSHTNGETHAFARVQDFTYDLDL  
 GSGVSATGVSGADGRAIVGSAVKTEGKIVGAFYAGEDHDLTLGGEARVDTISSDGL

[illegible]

CPH\_0799 905001 903940  
 no robust homolog present in Genbank/EMBL as of 11/7/98  
 KRENNAAIKQIKRLRSLSSQLLMMFLSYLSLGYCYITDKPEDQHTSSSAVKKDMHGK  
 TLRLSLNNKSAKSAVGTCACTVCFIKIDWTSYTVAVNNYWKTELPTSSVVKKSKSG  
 LSSDGGIAGLIVENELSSQFAVNNNNHMYLLPTSAWVSKAYGSLSDGVSVTVGEAKDA  
 RFTFAVTKVHGAEALPVGMHAKVANSVNSGATVIGVSDAGSILYAVKVEGRTITL  
 TLLCYSLAAKAVNSNGIKVIGRSTYTGVEAFHAFHGM:MSDLQCLDGGYSAAKQVSA  
 KTVICVHSTANGKLHAKFKVCGRSTIDLGESYWKACAAIIVSIDGELIVGVEG

Phn\_0900 906550 905249  
Eno-Enolase  
KKEIKIMFEAVIADICAREILDSRGYPTLHVKTTSCTTCEARVPSGASTGCKKALEPR  
TDCSPYRGCKVGLQAVNNKREILTPLVYKCGSVEDSLISLMDSDGSPNKKETLQANAIL  
VGLTALATAIAAATLRRRLPYLHGGCTACSLSPPHNNILITF73HMAODLLEFPFMRIPGA  
SIEKAVNNKAVDFMTLKLKLLERCGTLTGCGE77F4HILASNEALELLELALALBKAFCT  
KGLDGLALDAAKISFNWKTGTLTDRHIEEGIALILGLHLDRYTITLITENLAEALQGM  
TDTLVDLEKRVITNNLTFTNPTELLELISGLIFANLVIETNNITFTTTFYVAKLQAM  
TDTLITLIT73H73T7TTTITADLAVAFNAQIKTQSLGSPFVAKYNNIKELIPEELGKAT  
TDTLITLIT73H73T7TTTITADLAVAFNAQIKTQSLGSPFVAKYNNIKELIPEELGKAT

[illegible]

**PCT/US99/26923**

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PCT/US99/26923

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PCT/US99/26923

[illegible]







PCT/US99/26923

YBWS-1011D 310625Z (120101Z)  
PHUKSETLW118/PKAGMDJ/PF0LLKYAARA100KUNN1110VTT10EFT07  
FVEGVMVHYKAU2157EELKOKY07FIVEG1T0707V10707V10707V10707  
RLEELAK07FVTKL0707

[illegible]

CPn\_0917 1048054 1048539  
hydrolase/phosphatase nomolog  
PNDIILEVCTLVNNTKYEYSFGVPIPKFPGTPTDNTLKACF:CHTRGIWGGFPGKNSD  
KEGPOEAARELVEETGLSVNFFPKVLIEQYSFNTEDVTVRKVYTYFLAEVRGDINAD  
PWTGKQSGIATLITLILSEFPELRDLTVADKFINNYLPS

CPh\_0918 1049232 1048579  
ppe-Inorganic Pyrophosphatase  
ELMSKKPLVVAHPHSPPTLTCDNYEELSCYIEITPYDSVKFELDKATGLLKVDRPKFS  
NIFPCPLVGLLPQTYCGTASGVSGESTRRREGIGGDKPDLVCVLTEDNIHNGNTLQGAAP  
IGGLRIIDSGEADDDIIVLEDDLVFAIEDISDPCGTVLDRIGHYFTLYKATPAKILIG  
SPAKIEIVGVIYGGKEAGVPTQLAEDLVFTYDGTAEVN

cdh\_0919 1049375 1050430  
 lch-Leucine Dehydrogenase  
 PGLYSLAFKEIKIKIDYERVIE TSKSVRLHAIIAIHQVAGPALGVGRVLSYFEDACT  
 DAKRLARGHTYIAKISHTITGGGKSLVILIPDASPTEDMRAFGQAVNALGGTYTICED  
 LGVSDINISVLAETPTFGVGIADVGSDPSTYTHANGKPIKETAKYVGLGSSSLRGKKIK  
 QIGVSGRRLLSLPTFGAELVADVLEVDVQDAARLYCATVPTPEIHALDEGIDTFSFCA  
 RGRVIRKDLADLKCAVGVANQLEDSSAGHNGELVLYGDPVYLVAAGLLVAAAI  
 GRVYARERKLKLVETIPVLGKSYNSKTKGDLVALSDSPFDKLLAYTS

CPN\_0920 1051421 1050431  
 CysO-Sulfite Synthase/biphosphate phosphatase  
 ILKSGSLSEPNYQIVSVVETITLLNYSRHRLLPFKESGSGFITAAQDQSYT  
 LKQLAKAFNPVPIGETEYLPDQNEKPEILIKLTKLLTSVSGRDLLSTLVPPVPSPT  
 LPMVLPDICTGATITIRAFVAFLSLITYEYRPLSVWCAKYNTNLYSLAAKGLDSTV  
 LKMLDRRVYADRRKQDQFCESLAALNQOHNHAKRLGLSLKLPNTSPRRLVSEYKALV  
 AGDAVDHETIRYPTDSPARAMDHVGAFLVEAAGRVTDAAGAFLEYTKRESLVMSMAVI  
 LAGSDQETHETLAAALQNLNVNPTKILAL

CPrn\_09221 1051526 1052293  
 GELAGLKLARATTYEYHVTLLGVALLLKLVFPROVGEVDTLNINPKQGCLFLANHWAEVDPI  
 ILRLYVQPSRFLVPRVHVAEYLLKGLKRVWYFVSSVSTIPOLPVKROGSLERDHWCTYE  
 ASNALNKGSLFLVPSGRLSRTGKEEYVNOYSAYVLLHRRWGEQNVLRVVEGLGASPR  
 YKQNSTPKLGASPKFAFRALLRGITFPHKPRVKITLCQVDHFLKFOFPTQGLNITLAS  
 WFMGGDNEPIEVFYA

CpN\_0922 1053266 1053927  
 aas-Acylglycerophosphoethanolamine Acyltransferase  
 QGHRSSRLSTTRKLRLQDNRNRHNNHNLRLPGSTLEAFLLTSEHDGIDACTDGL  
 GSLSTRELRLALIAVLKVKFSEDRVRGHPGASPTAYTGFLLAQTTPHMSHGL  
 RELCAATLRIEVRVRLTSQFIKHLTSGGVFVFPDLMHEDVRKRLSMKRCILGLS  
 CSVPMFLAIKPGVSGSSDQDAVLLETSGCEIKPAVPLTKHNLNQLCAQLQDPMTO  
 DVMLEALPPFHAYGNSGGLFLNGHVMFASPNLKNULVEIDDKRVLTGCTPVPF  
 DYLLTKAGNSCLSESLRVVIGDGLKDTLYETKKLQPOLALYQGYGATGCSPISTI  
 TSSPKSECVNQLPEIDMVLIIKSETHIPVSGDGLTVRNGSVSGYLNHDSQFV  
 KRGSGPGLTGDGLHGPSGLFLGRSLRFVIGGDMVSLSEALSILHEDINQMDA  
 GSVLVCGIPGDIKGLLTFLTTLITHEVNDILKSAETSSIVKISYHMOVESIPILIGGR  
 DVSUNALAVSLFG

[illegible][illegible]

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[illegible]

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[illegible]

Ctn\_0980 1126988 1125504  
 \*similarity to Saccharomyces cerevisiae hypothetical 52.9KD protein

LKPKKPKKPKKPKPVYLTFSTKDKLSYCDIIFNCSKRPKPLNSDHFIDNSANFLKPA  
 FSTPSLSADSDHGLQDCMCAVFLDVKNIIFVFLVETMCPPIITVYSTKSDYLLP  
 NIKNRYDTQVPAQLSDGMKQDPIFLIEDKNIIPGASDKDKQCTITLKALQVITDGM  
 PLNTLVITDEEEKSSGLVFLTDKKKALRADYLLTVGGITSEKHPIVYSIGANGVPL  
 KLTEDKNDKNSGLVGLQIANTVNTSEILSSLDHNPDSITLIPDQDALPSDQWPL  
 LKPKDTLRLNEDGLTPFGQCYEYSPESALRPFTVINGITSCGYTGKFTVTPYRAT  
 VLYSLRVLPQDPAKAHGVTHLKKQVSPSLKSYLITLPGCSGRWSSANLPVTVKQV  
 YSLDYLNECLRLNPATPIGPIGLLEAAQTSPITCGTSTYSDIKAARENPHKQDLQK  
 LSYNCDLKLPKPKK

CpM\_0981 1127019 1129952  
Zinc metalloprotease (insulinase) (family)  
VTSEKAGCTITRNPIIKSKDLPETESKLEADHKPTGASIMHVNQEDNVNPHCFKPT  
POTNGVAVNLEKLVGCGSSDNPVDRPPTSHTRSLNLTINAFGTDPDFTYCPAASDIPOT  
FYTLSSVYIDAVPHLTITQSGFQKZAMRYEYENLNLCTQVFNVDKQAMNSGEARLS  
ALMAAIIPSVYITVGVNNGSDPREVTLSKEDVAFHQSQYSINRCLPYTYGHTKPIHDL  
LEEDLRKQALQKQVAGLQKRFKEPVNLTITVQVDEEDKLVPGISLCTSLDQ  
LEALVHLYITLTAGTDSPLSKRLSKGFCOTGNSINDEIRITPVLTKGSGSPAGAG  
LEALITFASLEETITRETSINTEVDGAVHGLSKRELTQYSLPYGLSIFPSGLLKQNGS  
AEDGLRHSLFSEKNSLJONSDYLAJKTRKYRLDNHFAVRVLLPDTLVAKNDKQDQIL  
LVSVEEDITDELKIQONVRELTSEQQEDKLIINLALQKLVYISDKEVPLKIKLS  
QGVGVAKHCFNDIVDFVDAVILPPLSGEELMLNLLVTLAKLQCGGSGSKIEHLEFL  
TQKVGQVSDYSPHANTNSLFSVSYIRGALSCKSKDGLVYNLSTVDFDTIPRIE  
LHQBZLALNTSVRSIRSYAVSNACSGNISITGANSYLITGLPYVKIKRELTFQNDQD  
EAVVYLQRLYLTQSGFKQKQITVSGSAGNQQQLKQDYGILLDYLITPFWENDEKAV  
TSGRLHITPARAAFNPAVFPQGIQZADHFNPAALTVAAEILDNVLYLHTIKEDQDAGSGA  
KAMLSRGSFYCYSPDRPEIAITTYTKLTVGVSELAGSNQDLYEGALGVQWDLNPAV  
SGRSVAFPLTKSGRIPLQVAFRRSLVITKEHTCHVKNRYLESTVQVLTISFAGZEH  
LQVLTITLDDPFPVPAI

[illegible]

CPA\_0983 1132045 1131206  
CPA-A-Glycerol-Serine Phosphatidylyltransferase  
NPNLYCYDQKIMQIMAGLQELANGKRRIVYTPNNAITAFGLCCGLFIIFKSVLRTSSVEL  
NHLGLGGLLISLISAKIADPSDQATARIMKAESAPQGLSDSVAWTPGPAITLAKIKELD  
NLYGVNFFSLLLTITSIYICGLVLRVYHNPFSKPTVDYKSPYCFIGLIPAAAAISIV  
NLIASLADFPDLPQALPQVGLSLLAFLLIGGLHISPKAFPGVKHPRFNVSSFTLVVYIGL  
ACLFPSGLGVHGVVEVFLVGLVLTGLVGPFIISITRYKKS

[illegible]

PL02985 1135432 1136571  
 ATGCG-Ribonucleoside Reductase, Small Chain  
 GAGGKQKQGNKPLGKGRRLRLITKRAKAEEDLGLKUKRVVSKGLLVNNGGV  
 LKLVLPVKKIKMAYHGLNACNANGLVPMVARDLNLNGLDESDERRVLLNLGQV  
 EICLVNGLNIVLAIFKIIITNFAORYLLHQAQFEAVITITFLYILNGLDDEEPPVNAV  
 KAKIIPAKDDQVHTITDITVDFHFTVQVGLVGLKGLVYVITLITLFPYDTPVNL  
 LKLVNGLVGLVYVILDITDITVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV  
 LKLVNGLVGLVYVILDITDITVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV  
 LKLVNGLVGLVYVILDITDITVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV

[illegible]

**PCT/US99/26923**

119

**PCT/US99/26923**

PCT/US99/26923

19

CPN 1042 DT 170602Z ED 5714C  
 "b10d-dechlorioeth synthetase"  
 NRSPPTTYPRANTFNRITIVGIDTGVGTIVGAILARALIAEYWKPIQAGKLENSDGNV  
 HELSGAYCHPEATYLRKPLSPKRAAIDNVSTESHICAPKPTTSL:ETSGGLFSPCT  
 KRLQGVDSFSSNCSTLVSAQVLGINTCTVFAHRSLN:LGHWVNGYPEDDGLT  
 OETKLITGLAKRIETKITSYDAQNKVMTSMRGLTGVSTPSLALH

[illegible]

CPn\_1044 1198700 1197699  
 \*b10b-Biotin Synthase  
 AKHKESTVSWSLDRTREIYHTVPVFLTHKAKALILRSNHLSELTCTYLTISTKGGVED  
 CAYCAQSSQVDTYTPRHKGLVHIDKQRAVELCATRVCLGAARHAKQDDYFPRVLA  
 MYKSLTDLGAAYVCCALGKLSZEQAQKLYDAGLYAYNHQLDSSPEPYETLTITRSYEDRLN  
 TLVDVNGEYLTSTCCGQVNGHGESEDRLEKGLAVLATRQHLIPESVPVNLKLPIDDTQGP  
 PPISVTEVGLTATARKVYFPRSHVRLHSLHLYVDQDTCLAGANSLPYGDKLTVEH

CPn\_1045 1199602 1198901  
\*conserved hypothetical bacterial membrane protein  
GDVPHSTSHUKTLYVSYLSTSTTLLVLNLVLSSKLIPTTTFNIPGGLTLYPLTLLI  
STLNEFLIPGPKAKRVTISAFANLKLASSIVQIPHTFVVPASPEHQTAHMLFDLSPLAFL  
ASLALFTVSGQLDLYLTFTFNKTPSSMLALRSNGSTWISOIPDTFIVTCLILFYNGLS  
FPTNLNDYSLTITKTCVLTPLLYAVNTIPKGLQSPSTKIANVTLNDQP

[illegible]

CPN\_1047 1200537 1201343  
cdapc-Dihydrodipicolinate Reductase  
PGSRMGSSGVGVGCGSGRTGKVTYSALEGDSSEYTLGPGFSRSSALTLPQVIAHNDVIV  
VQSPHILLTKEVVAHLLISPKPLIGITGTGPGKGLKANDSLEELTHVPPVWNAHSLGIA  
IHKRLVLLSQQLNPQFDITRTREHYKQDLSGTAGDQLDTIQOVQKEDNGEETVGG  
RDSKIKTIEVGSRVGDIPGHEVAFISGEGILVRHTVTVSNVYFCRGLISILNDLMLN  
PQGLYSLLVNDLVLVRNEDLKLKTTD

CPA\_1048 1201588 1202604  
Asid-Aspartate Dehydrogenase  
CGEGRKGRITAVLGLGVLGVKLVFVLAHWKRDYVAEYVASNKYGCGYGDACINQKPT  
FVGRVNDLPRLKRIKEZGVDFVSLFPPSSAEHMAVLSQGVVVFVNATYVRRHVSFPI  
FVGVNSHDFGVLFLEEDPVGKZITSNPKVGLITLALAPRLSLDNHNVITVLOSAGQY  
GQVPSVLDLLANTVPHVIGEXKILRLTVKVLGSSKQVPCKLVSFVHRVVPVAYGHTLSL  
VPTYSKLVDELILVLSYOEKNGEPFNTYGLVYNPVSPOAKHLSKDDNRVVLGPITYGDF  
TIRHGVILVNLVRLVAGKGLISFNRVYEVYVSRNCIRI

[illegible]

CPRL1050 1203884 1204798  
 MGA-Dihydrodipicolinate Synthase  
 CHTKSYSRHVRIMHLLTATVPTFFNGTIDFASLERHLLSPQDAVNGVWLLGSGEGL  
 LLTKKEKALCFACADQLQKPLVPGTSGTLLKVLWLLFQDGLPTGISGFWTLPTVTKP  
 LKGGDTLHFVAFLNAKQKVPFLTNSPAAKGLPLVDYKALAHVFLGFLIKSGGSEVEET  
 STKSTAPHLFVYQDDPTFENACRAATLSVLNNAWPEARYGVWLLPQEQDQVSLNM  
 TCRWVWTTNPTTGIKATLAYKAKITRAHQRLPLGIEDFDLENVSPAVESHAWPKLRTS  
 YFSYS

CPn\_1051 1204956 1205270  
No robust homolog present in Genbank/EMBL as of 11/7/98  
FHTPKSIQQLHLIKTIDPVKISPVTTKSSFFRQSLRLRFLFMHLYCINSIRNFCV  
IATTFICRGLILFLTTLFSLNHCILHFTLTPWICKEDPRIIRNKK

Pn\_1052 1205402 1206169  
 no robust homolog present in Genbank/EMBL as of 11/7/98  
 FIDQKQNSREKIKALR(LKSGITVFRNGLGSGYDKITFYGLSYVFNQIPNSIGCR  
 FPFPRPKTEVEINPKF(KDEIDPLFINDIVKVEGFPPFKAALDELSSGQISGNLA  
 SNFDFLRALNFKFKEIKMTITFLKQNTVDSSEPTFATYINLVKSLGKSGY  
 VADGLKRLKEDVDSIRTRATSLVWIKSVIRPLPLTFYIWKRPILFFRITSD  
 TRDLKKFRLEIKD

120610Z 1206101  
FM JCRC J3 J4 J5 J6 J7 J8 J9 J10 J11 J12 J13 J14 J15 J16 J17 J18 J19 J20 J21 J22 J23 J24 J25 J26 J27 J28 J29 J30 J31 J32 J33 J34 J35 J36 J37 J38 J39 J40 J41 J42 J43 J44 J45 J46 J47 J48 J49 J50 J51 J52 J53 J54 J55 J56 J57 J58 J59 J60 J61 J62 J63 J64 J65 J66 J67 J68 J69 J70 J71 J72 J73 J74 J75 J76 J77 J78 J79 J80 J81 J82 J83 J84 J85 J86 J87 J88 J89 J90 J91 J92 J93 J94 J95 J96 J97 J98 J99 J100 J101 J102 J103 J104 J105 J106 J107 J108 J109 J110 J111 J112 J113 J114 J115 J116 J117 J118 J119 J120 J121 J122 J123 J124 J125 J126 J127 J128 J129 J130 J131 J132 J133 J134 J135 J136 J137 J138 J139 J140 J141 J142 J143 J144 J145 J146 J147 J148 J149 J150 J151 J152 J153 J154 J155 J156 J157 J158 J159 J160 J161 J162 J163 J164 J165 J166 J167 J168 J169 J170 J171 J172 J173 J174 J175 J176 J177 J178 J179 J180 J181 J182 J183 J184 J185 J186 J187 J188 J189 J190 J191 J192 J193 J194 J195 J196 J197 J198 J199 J200 J201 J202 J203 J204 J205 J206 J207 J208 J209 J210 J211 J212 J213 J214 J215 J216 J217 J218 J219 J220 J221 J222 J223 J224 J225 J226 J227 J228 J229 J230 J231 J232 J233 J234 J235 J236 J237 J238 J239 J240 J241 J242 J243 J244 J245 J246 J247 J248 J249 J250 J251 J252 J253 J254 J255 J256 J257 J258 J259 J260 J261 J262 J263 J264 J265 J266 J267 J268 J269 J270 J271 J272 J273 J274 J275 J276 J277 J278 J279 J280 J281 J282 J283 J284 J285 J286 J287 J288 J289 J290 J291 J292 J293 J294 J295 J296 J297 J298 J299 J300 J301 J302 J303 J304 J305 J306 J307 J308 J309 J310 J311 J312 J313 J314 J315 J316 J317 J318 J319 J320 J321 J322 J323 J324 J325 J326 J327 J328 J329 J330 J331 J332 J333 J334 J335 J336 J337 J338 J339 J340 J341 J342 J343 J344 J345 J346 J347 J348 J349 J350 J351 J352 J353 J354 J355 J356 J357 J358 J359 J360 J361 J362 J363 J364 J365 J366 J367 J368 J369 J370 J371 J372 J373 J374 J375 J376 J377 J378 J379 J380 J381 J382 J383 J384 J385 J386 J387 J388 J389 J390 J391 J392 J393 J394 J395 J396 J397 J398 J399 J400 J401 J402 J403 J404 J405 J406 J407 J408 J409 J410 J411 J412 J413 J414 J415 J416 J417 J418 J419 J420 J421 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J1018 J1019 J1020 J1021 J1022 J1023 J1024 J1025 J1026 J1027 J1028 J1029 J1030 J1031 J1032 J1033 J1034 J1035 J1036 J1037



PCT/US99/26923

122



WO 00/27994

PCT/US99/26923

51

cDNAs				
cDNA #	Begin	End	Type	Codon
1	89657	89728	Thr	GCT
2	90998	91070	Tro	GTA
3	91070	91141	Met	ATG
4	91141	91212	Met	ATG
5	296075	296147	Val	TAC
6	296151	296224	Asp	GTC
7	409848	409922	Pro	TGG
8	462141	462214	Arg	GCT
9	672236	672318	Leu	CAA
10	677264	677337	Arg	TGG
11	739403	739486	Leu	CAG
12	781610	781680	Gly	TCC
13	784822	784896	Glu	TTC
14	784922	784994	Lys	TTT
15	836119	836191	Ala	GCG
16	843926	843999	Pro	GCG
17	877400	877473	Arg	AGG
18	1085605	1085676	Gln	TTC
19	1142034	1142118	Ser	TGA
20	1175863	1175944	Leu	TAG
21	1230028	1229942	Ser	CGA
22	1137462	1137389	Val	GAC
23	1030603	1030533	Cys	GCA
24	1000022	999949	His	GTC
25	961607	961536	Gly	GCT
26	807413	807341	Arg	TCT
27	786780	786708	Thr	GCT
28	715971	715889	Leu	TAA
29	708441	708354	Ser	GCT
30	680259	680178	Leu	GAG
31	631445	631373	Phe	GAA
32	626987	626901	Ser	GGA
33	293477	293405	Thr	TGT
34	293399	293317	Tyr	GTA
35	269142	269070	Ala	TGC
36	269065	268992	Ile	GAT
37	164389	164318	Asn	GTT
38	87522	87450	Met	CAT

WO 00/27994

PCT/US99/26923

## What is Claimed is:

1. An isolated nucleic acid encoding a *C. pneumoniae* protein as set forth in Table 3.  
5
2. The isolated nucleic acid of Claim 1, wherein said nucleic acid has a nucleotide sequence of an open reading frame in SEQ ID NO:1.
3. A probe comprising a hybridizing fragment of an isolated nucleic  
10 acid according to Claim 2.
5. An isolated nucleic acid that hybridizes under stringent conditions to the nucleic acid sequence of Claim 2.
6. An expression cassette comprising a transcriptional initiation  
15 region functional in an expression host, a nucleic acid having a sequence of the isolated nucleic acid according to Claim 1 under the transcriptional regulation of said transcriptional initiation region, and a transcriptional termination region functional in said expression host.  
20
7. A cell comprising an expression cassette according to Claim 6 as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell, and the cellular progeny of said host cell.  
25
8. A method for producing a *C. pneumoniae* protein, said method comprising:  
growing a cell according to Claim 7, whereby said *C. pneumoniae* protein  
is expressed; and  
30 isolating said *C. pneumoniae* protein free of other proteins.

WO 00/27994

PCT/US99/26923

9. A purified polypeptide composition comprising at least 50 weight % of the protein present as a *C. pneumoniae* protein comprising an amino acid sequence of claim 1.
- 5 10. A monoclonal antibody binding specifically to the polypeptide of Claim 9.

WO 00/27994

PCT/US99/26923

Contig463

Length: 273254..

1 ATTGTTCTCTG TAAGAACACT TCCAAAGCGC ATTTAATCAT TTTTAGTAAA  
51 AAATAAAAAT ATACTTTTAA ATGTTGAGAA AATTTTTAGC TAAACTTTAT  
101 AAAGGGTTGT TGGTGAAACC TTTGGGTTAC TCCTCAGAAC GACTTTGTGA  
151 TTCTATAGTA TTAAAAGGAT CTTGGAGTAT AACAAGTAAA GATCTTTGAG  
201 GATAGCGTAG GGCCGTATTT TGAATAGCGT CCAATAAAGC GCGTTTGCAA  
251 AACGCTTGAG TTTGGTTGTC CCAATAGAAA GTGCCTTCTT TAGGAAGAAT  
301 CTCTTCTGGA GGCACCTCAT AGACCGAAGT AAAGAGAGGA AGAGCAACGA  
351 TTGCTGCATG ACTTTCTATA GCTGCTTTAA GGCAGTTCTC GTACGCTAGT  
401 AAAGCTTGGC GATAATATTC TTGCTGATTT GGTAACCTCT CAGATTTAGG  
451 GCCGCATACG TGGCCTAAAA AGGTCGGAAG AATACTTTTC TTTTCTGCAG  
501 AGCTTAAATT TAGATTAAAC GTTTGATCTA GAGCTTCGTT TGGAAGTTTT  
551 ACTACTCTCA CTTCGGTAGG GGAAAAGGGG TCTTCTCCTT TTGCGGGACC  
601 CCCTTCGCGT TGCTTGCATG TATCCACAC GCTTTTATCT TTTAGGGTGG  
651 AGTAAAGGAT AGTAGAGAGG TTCGTTGCAG TGTTGTCGAT CAGATTCGTT  
701 GGGCCTACGG GATTAAAGAT GATCCCTGTG GATTGATTTT TTTCGATCAC  
751 TCTAAGTCCA GTTAAGAAAG TAGGCTGAAA TGGTTGAGAC GCATCTGTTT  
801 GTATCGCTAC CTTGAACTTA GGGTTCAGGT GATTATTGTA AAATTGCATC  
851 TCGTTTGAGT AGCAGTCTAC GTTTTTTTCT TGCCACGCTT TTCCCAAAGG  
901 CTTGAAGTTT TGCTCTAGAA CTTTCTGCCA GTTAGAAGAT ACCTTTGAGG  
951 TCATTTGGTG GTAGACTAAG AAGGTTACAA CTGAGAAGAG GGCCGTGGTA  
1001 ATGAGAAGAG CCAAAAATAC AGGGTTCCCT AATACTATCG TTAAAGAGAT  
1051 TCCAGCCACC AAAGCTCCTA AAGCTAAAGA AGCTAGGATT GCAAGAGTGG  
1101 ATATTTTTGC TATGGTAAAC TGTTTTTTAG GAGCAATTTT TTTATCCCGA  
1151 GGCACATAGG ATAGTACAGA AACTTGAGAG CTCTCAGTAC GTGAGGGTCC  
1201 TGACATAACA TTTTTTTTGT AAAATACTTT CTATAATTTT AACATATTTG  
1251 TGTTTATCGA TCCGAGAAAA TTGGAGAGTG AGAGCGCATG TCTTGCAATT

WO 00/27994

PCT/US99/26923

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1351 TGGGAGCAAA TATAGCGAGA TATAAAGTAT AAGGGAATTG CTGTTAGGAA  
1401 GATAAAGGAG CACAAAGGGT GGATACATAG CCCAATAGCT ATGGTGGTAG  
1451 CAATCAGAGC TATCCAGACG AGTGCAATCG CAATAGTAAC GAAGAGGGCA  
1501 AGCTTGAAAT TATAGCGAGG ACGAGTAGCT GGGGGAAATA GAGAGGGAGC  
1551 CGTTCCATCA AAACCGGGAG TAGCTGAAGA AGCCATAAAC TATTAAAAAT  
1601 TAAGTTTTTT TCGGAGCATA AAGCATTTTA AAGTAGTGGG GTCTTTTTTG  
1651 TCACGGAGAT GTCCTGGACT TCCCAAGCGT TTCTAACAAA GATACCTGCT  
1701 TTTGAGAGGA GAACTTTGA AACTCCTGCA AGGTCATCCT TCCTTGGCAC  
1751 CAGTAGGTTT TTTCAGGAAA TCGCGGAAAG ATTTTGCGA AAGCTCTTAC  
1801 AGTTGAAGGG CTTGTGAAGA TAATTTTTTT GTATTTAGAT AAAATATTTT  
1851 TTTTAAGTTT TCGCGGCTTC ACTGTGTAGT GAGGGTAAGA GAAAAAGTA  
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1951 GGGGTAGAGA ATGCGGGCTG AAGAGGGCAG TGCCTGTAGC AATGGGAAGA  
2001 TGCCTTCAGC GATTTCTTGA GTTGCTACTA CGTACTTCAC TTGTCCAAGG  
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2151 GGTGAGTGGG TGAGGGACTT GTGAGAATCA CATGGGTGTC TTGTGGAAGG  
2201 AATTGAAGAG CACGCTTATT TTGTGGAGTG CTTTTTGCAT AGGGGAAGAG  
2251 AGTTAGAATA GGCAAATAAT GAGCTTGGA TTTACGAGCG GTTTTTTGAT  
2301 TCAATCCTAA GTAGAGGGTC ATGAGTCTTT TCGGGTAAAA GGAAGGCTGC  
2351 CTAAGTTTTT GTACCTTCAA AGGGATATAT TGAAAATAAT TTTTCTTTTT  
2401 CCCTTGGTTC TTCTTGATCA TCGGTTGATT GACATTTTTC ACTTTGAAGG  
2451 CTAGGCTGGT TTTTCTGGA CTTAGAGGTT CTCTCTATTA AGGCTTCGTC  
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2601 TTTAGAAAAT GCTTCGGGGA AAAAGGGACA AAGTTTAGCT TCGACAGCGT

WO 00/27994

PCT/US99/26923

2651 ATTTAGCAGC TCTTGACCAT CTCTTAAATG CGTTTCCTTC CATTGGGGAG  
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WO 00/27994

PCT/US99/26923

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5201 CCAGTTGCGC GTTCGTACTT ACGAACGTGG AGTCGAAGGG GAAACTGCAG  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

8051 ACACCACATC TGGGGTTTCA GAGGCTGCGG CGGCTGAGGC TGCCGTGGAT  
8101 TCTACACCAG GGACAGAGGA GGAGCCGAGT TTTTCTCTGA GGTATGCGCT  
8151 TG TAGTTCAA AATGTTCCCT ATCCAGAGCC GCCTAAAGAA CCTGAGGTGA  
8201 TGTTTACAGA TGAAGAAAA AGTCTGATTT TAGAAGCTAC TCGTGCGCGT  
8251 CGTATGGAGT TGGACTTGTA TAATGGCTAT TTAGCTGATT ATGAAC TTCT  
8301 TAAGGATGAA ATACAGAAAC ACGTTCCTGA TTTACCTGAG AATTGGCGTA  
8351 CGAATTGGCG TTGGTCGGAG AGGCTCTATA AATTTTCTT TAAAACAAAG  
8401 AAAGAAGGAT TAGAAGAAAT TTTCTTAAAC AAAGAGTTAG GGAATATGAT  
8451 TCTTGCCCGA GGGCTGGCGG CAACTCAGTC ACAAGCACGT ATTAAAGTAT  
8501 TCAATTCTTT AGTGGCATGG CTCTGCAAA GCTTTAACGT AGGGAGGAGC  
8551 TGTACAGCTA AACCTCTTCC TACGTCAAAA CTAGACCTCT TTAAATCGGA  
8601 ATTCGAGTCT AAGCCTAAAA ATAACATCTT AACGGAATTT TTGGTGGCCT  
8651 CTGATGAGGA GATTCTCTTT AAGGGGCTAC GGGTCTAGA GCCTGGAATC  
8701 GAAGGTTGGT ATGACCATCC TGATCAAGCT GGAGAGATTC GGTGGTACT  
8751 CGAGGGTCTG GTGCAGGCTG GACGTATTTC TGGATATTGG GAGAATCAGC  
8801 CGTTTGGGAG ATTTGTCCTT AGAGGAGTTG GTGAAAGACG TACCGAGCTT  
8851 GTAGAGCTTT TGGAGAGTTT AGTTGCTTCT GGTGAGATTA TGCAGTTCTT  
8901 TGAGTCTTCG GATGAAGAGG GTGCTTTTAT TATCGATAAC GAACCTAGCA  
8951 AGACTGCTAT GCTAAAACAG CGATTTAAGA GTTGTGTCAG GACGAAGCTT  
9001 GTCGGGAGTT TTGCTGATGA GAGTCTTCCC AGAGGTAGGT TTACCATTTT  
9051 AGTTTAGCGT GGGGTAGAGC ACTCCACGAA TCTTAGGGAG CTCCTTGCGA  
9101 CCAAGCTTGG AGATCCTCCA TGTTTTATTG TTTCTCTAGT AGCCAAATCG  
9151 TAGCCGCTCC TAGGAACAAT TTTTCTTTT TCGCAATATA AAATCCTGAT  
9201 TTAGAGAATA GGTCTTCAAG ATCGTGGTCC TTTGGAAGTT GCTGGATACT  
9251 TTTGCTGAGA TAGCTATAGG CGTCGGGATC TTTAGAAACA GACTTTCCAA  
9301 TCCAGGGGAC GACAGCACGC AAATAGAGCT TATGGGCACT ATAGGTAGGG  
9351 TGTGTTTTTT TTGGAGGTGT GAGCTCTAGA ATGCCAGTT TTCCAGAAGG

WO 00/27994

PCT/US99/26923

9401 .CATAAGCACT CGGGAGATTT CTTGTAGGGC TTTATGTGGA TCCGAGAGGT  
9451 TCCTGAGGCC ATAGGCCATC GCTGCTAGGG GATAAGAATG ATTCTCCAAG  
9501 GGCAGTTGAT TAATATCGCT ATGAATAAAA GAGCAAGAGC CCTGGGGAAG  
9551 GTGTTGTTTT GCAATGTCGA GCATTGCTGA GGAAAAGTCG ACGAGAGTTA  
9601 CTGATGCTTG AGGGTGTGCG GCAATATAAC GCTTCGCGAC TTTTCCTGTT  
9651 CCTGCGCAGA GATCCAGGAG AGAGTATCCC GACCCTAGGA TCTGGATCAA  
9701 AGAGCGATTC CAGAAATGGT GCATTCCTAA AGAGAGTATT GTATTTGTGC  
9751 GATCATACTT ACTCGCTATG GAATCGAAGA TCTTTTACA GTCGGGCTTG  
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9851 GTTCTTCTCC TAGACGGTAC TGGCATAGGG CATAGTATTC TTGAAGAAGA  
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10601 GATGAGGGCC GCCATTCCCT CAGCGTCCAT TTTAATAGGT TCTTTAGATG  
10651 AGGCCATCTG GAAAACCTTT TCCCCATAT GTGTTGAAGA AAGGTCATTA  
10701 GCACCACAGG AAAGGAGGTC TAGAGCTGCC TCAATACCTA GGTAATTCCA

WO 00/27994

PCT/US99/26923

10751 TAAGGCTTTC ATATTGGAAA AGTTGTCTAA GAAGATTCCG GCTACTGCCA  
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10851 TTTCTAGGA CATTATTTTC TTGGGCGAAT TTTAGAAGTA TGAAGTTTTT  
10901 AAAGCCCTGA GTTTCGTCTT GTAAGTCGCG GACTTTTACC ATGTGGGTGA  
10951 CGAGGTCTTC AGGTCCTTCT TTATGATAGC AGAGCATGGT TATATTGCTA  
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11151 AGAACATCGC GAATAGAAAG GTTATCAAGA TCTGAGAGAT AGGCATATTC  
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11951 GACCCTGAGA TAGTAGAATA CAAAAGGTGC TTTACCGTTT GGATCTTTTA  
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12051 TTGCTATCGG GGAAGAAGGT ATGGAGAACT TCGCCATTGC GGATGATTTT

WO 00/27994

PCT/US99/26923

12101 TACAGTCTTG AGTAGGGCAG TGCCTGCCAC ATGACCAGAG ATGTGACGGT  
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12201 GCTGAAGTGA TGTGAAGCT TAAGACGATC CTAGGTCCTG TTGTAGCGTA  
12251 GCAATGACGT GCGAATAAAG CTTCAACAAG AGACTCTCGG GTATATTTAT  
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12451 CGCTATCTTT ACCTTGGATA GGAAGGGGT TGTTCAGAGC GGCTGTGGTT  
12501 TCTGAAGATC CCCAGGCATT ATAAATTTCT ACAACTCTTT CGAACTCGGG  
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12901 TACAAGTTTC AATATTTTCT TCAGAGTCGA CGCGTTCGGA TTCGCCGTGG  
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13051 AAATTCCAGG CTCATTGAAA TAGAGATTAG GAAGAATAAC AAAGCCTGTT  
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13151 AAGCTCGATT CGGGTCTCTT CAGGAGAGAA GTTGGTGAGG TTCCCGAATT  
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13301 AGAGAAGACA TCGGGTTCAT CATAGTTTCC TTCTCCTGTA GGATCGATGT  
13351 AGAGGTAAAA GGGTTTGCGA CGTTGTGCGA AAAGTTGGGC TCCGTTCCCA  
13401 GCATCATCGA CTTGAGGATG GTTTGGAGAG GCTCCCATGA CAATAGTGAG

WO 00/27994

PCT/US99/26923

13451 GGTTCCTCCT ACTTGAAGTT CGTAGGGGAG AGTAAACTCG AATTGTGGAA  
13501 CGGGATTGTC TTTTACAGGA ATGGCGGTTG CTTCGATGAT TTCGCCCTCT  
13551 GGCATTTCTG CGTAGATTAC GTTCTAGTT TGGGAGAGAT CTGTCGCGGG  
13601 GGCTTCCCAA TCTGTGGGTT TCCCACTTCC TGCTAAGTCA AATTTACATT  
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14451 GGAACAGCAC CCACTTTATG GAAGACATGT CCTCCTAGTG TATCGTAGCT  
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14601 TTTTCTGTA CGTCGTGCTC GTCTGCGATC TCTCCTATAA TTTCTTCGAT  
14651 AATATCTTCC ATGGTAGCGA TGCCTTCTGT GAATCCGTAT TCATTGACTA  
14701 TGATGGCTAG ATGGCGATGT TTTGTGCGA ACTCTTGGAG AAGAGAGGAG  
14751 GCTTTTTTTA TTTCTGGGCG ATAGAATGGG GGTTTGCTAC TGAGGATATG

WO 00/27994

PCT/US99/26923

14801 GGTGGCTGA GGTCTGGCT GCTTGATAG AGCAGTAAGA GATCTTTAAC  
14851 AAGAAGGATT CCTGTGATGT TGTCTAAGTT TTTTATATAA ACGGGAACGC  
14901 GACTGTAGCC TTCTTCGCTT ACGAGAACCA GAGCTTCTTG TAGTGTAGTT  
14951 TCTTCGGGAA GTGCGAAAAT ATCTACTTTT GGGATCATGA CTTCACGGAC  
15001 AATGAGGTTA TCAAAAGCGG AGAGGGCTTC GGAGAGCTGG CTTTGAAATG  
15051 ATGTTGAAGA TCGTACTTGT TGTTAGGGC GCGCTCTGTA AAAGAGCAGT  
15101 TGCAGTGGGA AGAGACCGAG TTGGAATACC GAAGCTAGAA AACGGAGGTG  
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15301 TCCATAGAGG ATGCAGAGCA GCGTGGCGAG AATTGTAGGA GCACTGGGGA  
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15701 GCTAATGAAT GCTTCTCCTA AAACATGAGG ATAAGCGGGA TCTCCGGGAG  
15751 CATCAATAGG CAGAGTGATC GTATCTGTTA GAGAAGGATC AGCAAATACC  
15801 TTATCATGGA GTTCTGCAAG AGCTTTATCT TCTAGGAAGT AGATAAAAAT  
15851 TTCATTAGTT GTTACTTTTA AGTGCTCTAA GAGCGTAAGA ACCAGCTTCT  
15901 CTACAGAAAC CAAATGAATA GGAATACATG TTTGCTCATT GGAAACATGT  
15951 ATTTTGATCT TTTCTTGCCT CACGCGAATG AAATTCCCAT AGAGAAAAAC  
16001 AAACCTATTT TAAAATAGGG GTCTTAGGTA AACCTGTGAC TTTTTCGCT  
16051 GTACTATCAT TCCAACGGCC CAACTTACGC AAGACTTCTA CTCGCTCAAA  
16101 ACGCTTCAAA ACATTTCTTT TGTAACCCC TTTGACAGAT TTACCATAAC

WO 00/27994

PCT/US99/26923

16151 TACGATGTCG AGACATAATC CTGCTCTAGA AATAAACCTA TTTTCGGGAT  
16201 AAAAATGCTA TCACTGGTGC TCAATGCATT CGTATGCAAT TTATATACAA  
16251 TTCTTGGAGC TGGCGCTGGA TGCACAATGG CATACTTAGG TTTACGTTTT  
16301 TTAGGACTTT TCGCTCTGCG CCGAGCTTGT TTA CTCTCATTG GTGTCATAAA  
16351 TAACTCGATA TTGAATTTTT TAATTTCTCC AGACAACGGA AATTGAGGAT  
16401 ACGGAGTACT TTATAAGAAA AAGGATAGTA AAAGAAGAGT TTTTTTTCAA  
16451 GAAGATGACG TCTTTTAGCT GCCTTGATCT TGGTGTAGCT CGTCAGGGAG  
16501 GGGAGACGAG GGGCATGCCA TGGGGGTTGA GAGGACTCCA CAGGAGATAA  
16551 TATATTTGAA AGCATCTTCG ATTTTCATAT CTAGGAATAC GATATCAGAT  
16601 TTTCTAAATA GGGTAAGAAA CCCTGAGGTG GGGTTGGGTG TTGTTGGGAT  
16651 GAAGACCGTG ACGAGGGGGT CGTCTTCCTT TTCTCCTGTG CAGCATACTG  
16701 TGGGTGCGTC TCCAGCGACG AGACCGATGC ATTGAACATT TGCCTTAGGG  
16751 AAAGGAACCA TAACTACTTG TTTGAAGGAT CCTGATTTTG ATCCAAATAT  
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16901 ATTCTCGTGA GGAAACCTAG GAGCACTGTG GCGAAAAAGA GACCGAAGAG  
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17101 GAGAATAACA AGTCCTGTAA TAAAGTATTT TTTCATGATT CTCCTGCAAG  
17151 ATATGAGGAA ATGGGCATTT GTTCTTTTAC TATACAGCTT AAGATTATTT  
17201 AAGATAAAAC TTTTCCCGAA TCTTCTGGGG ATAGGAGAAA TCTCCATGGG  
17251 ACATCACGAT ACTCTTGAGC ATAATCGATG CCGATCCGGG CAGTTGCTGT  
17301 TAGAGTCCCA GAGATTTTTT CTTTGCTGAT ATAGAGAGCT GGGGTATTTA  
17351 GGCGTTGCCT ATTGTTTTCC AAAGAGATTC CTAGAGCTTG GCACACTTTT  
17401 CCGGGTCCAT TGGTGAGAAG GTGTGGGGGT TTATCTCTCC ATTGGCGGGC  
17451 TTGGATCATA AGTTCTTTGC CTTGATCAGG AAGGATGGCC CGGATCAGGA



WO 00/27994

PCT/US99/26923

17501 CGGCATGGGG AATGTCCTCA GGTCCAGTGA CAACATTCAA TAGGTGATGC  
17551 ATGCCATAGC AACGGTAGAG GTAAGCAGAG CCTCCTTTCA GGTACATCGC  
17601 TCTGTTCCCTC TGAGTTTTTC TGTAGTTGTA GGCGTGGCAT GCTTTGT CAT  
17651 CAGGGCCACG ATACGCTTCG GTTCTACAA TGTAACCTGA AGTTATCAGA  
17701 CCCTCATGTG TTGTGATGAG TTTATGTCCT AAAAGCTGTT GCGCTAGTGT  
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17801 CTTTTTTTCG TTCCTTTTTT CTTAGAAGGC GTTTTCTTTA TTTTCTTAGG  
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18501 CTTGGAAGGC GAGTAGGTTT TCATCATTGG GAGGTTCGTG ACTACGAAAA  
18551 GG TAGAGAAA CGCCTTGATG GGAGATATGA TAGGCGACCA CTTGTTTGC  
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18751 TTTACTTAGA GTGGCCATCT CATTGAGGAT TTTTGAGAGG GGGTGGGAGT  
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WO 00/27994

PCT/US99/26923

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18901 TGTAACGTC ATAAATACGG ATACAGCGAG TCTATCAACG TTTGGTTTTA  
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20101 GTCGTTATCA ATAATTTCTA CATCAGCTTC TTCGATATGG TCTTCTGAAG  
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WO 00/27994

PCT/US99/26923

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20251 TGCTGATGCA GACTGCGATT GCATAGACTC TCCAATTTTT TGCATATGCT  
20301 TGCTTAGGTC TTCAGTAACC TCTTTAATTT TTTCAATAGG AGCGTCATCT  
20351 TTGAGTGCGT TGCGCACGTT TTCGATTCGC TCTTCGATTT CTTTAACTAA  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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34951 CGAGAGTTTT TTCAAATGGG AAACGAGTCG TCCGTCTGGG GAGGCTGCAT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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88651 CAAGAACATT GACAACCGCA TTGTCAGTAA TCTTCAGTTC TCCACTAGCG  
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WO 00/27994

PCT/US99/26923

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89201 GATGTTGCAG GTTTCGGCGT AGATCGCACC CGCATCATTT GGTGTACCAT  
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90301 CCCTATAGAG GTCCACGTAG CTCCATTAAT AGGTAATGTC GTATCGCAAT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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93001 AGTAAACGCT GTTGAAGCAA AACATGGCGC CAGTGTGGTA GAAATTAAGA  
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WO 00/27994

PCT/US99/26923

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94251 TTCACGGATA TAGAGATCGA TCCTCCAGGA GCAATGGCAA TGGCTCCTCC  
94301 ATTACTATTC ACGTCATGAT AAGCATGATT ATTTTCAAAA CACGAAGGTC  
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94401 TGGCTCACAT TGTCTCTAAA CACCAGGTAG CGGTTCCCGC TGAGATTTAC

WO 00/27994

PCT/US99/26923

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94601 TAGAGGTGCT GAGGTGAACG CTAAGTAAGA AAAATTAGAG AGAGTGAGAG  
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95751 GCAATGAGGT ATAGTGC GTT TCCATACGGT TGTCTGAATG GCTGAACGAA

WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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97301 GCATTCCCTT CAAAATATAG AAATTTGTTG TTCGATAGTA TCGACGTGCC  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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102151 AACAGTTTTT ATGGATCCAT AATTAGTGA TGAAGGATAG ACCCGAGGAT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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114601 TCCAGTTAGA GTACATTTGG TAGCATAGAT CGCACCACCA CTTACTGTTG  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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154051 TTTATTTTCA GCAATATCTT CAGGAACATC TTCAGGGCTA TCAAAACTTG  
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154201 GTAAATCGGT ACCCATGTTC CTACAATAAT CGTAGCTCCT GCTTCTGCAA  
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154501 AACTTCTCAC TCCCGCGTAC TGCTAAAAA ATTTTCAAAA GAATTTACGA  
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154751 GCATCCGGAG CCTCTGCATT AGGACTTTCA CCTGATCAAG TGCAAGCGTT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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160551 AAAGAAAAAA ATAAAAACAA GCAAAGAGAC CGTCTCAGTT TTAGTTTAGA

WO 00/27994

PCT/US99/26923

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160701 GCTGAGATCA CAGAAAAAAT AAACCACTTC ATGACTACCT CTGCAAAAAAG  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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167051 TCTATATAGT ATCTCGTGTA CTATGCCGAG TATAACCGAT CGGCGTTATC  
167101 GATGAGAGTT TCAAAAAAAT ATAAAATCCA CCTAAAGAAA AAGCGATAGA  
167151 GAAGGTTCGT ACATGACGCA TCAAGTAGCT GTCTTGCATC AGGATAAAAA  
167201 ATTTGATGTT TCGTTAAGAC CTAAAGGGTT AGAAGAATTT TATGGACAGC  
167251 ATCATTTAAA AGAACGCCTA GATCTATTTT TTTGCGCAGC ATTGCAACGA  
167301 GGAGAAGTTC CAGGACATTG CTGTGTTTTT GGACCCCCAG GCTTAGGGAA

WO 00/27994

PCT/US99/26923

167351 AACCTCACTT GCTCACATCG TTGCCTACAC CGTGGGGAAA GGGCTGGTCT  
167401 TGGCATCAGG GCCTCAGTTA ATCAAACCCT CGGACCTGTT AGGACTTTTA  
167451 ACTAGTTTGC AAGAAGGGGA CGTGTTTTTC ATCGATGAGA TCCATCGTAT  
167501 GGGGAAAGTT GCTGAGGAAT ACCTGTATTC TGCAATGGAA GATTTCAAAG  
167551 TCGATATTAC TATAGATTCA GGACCCGGAG CTCGCTCGGT CCGTGTGCGAT  
167601 CTTGCTCCTT TCACTTTAGT GGGGGCAACG ACTCGATCAG GAATGCTAAG  
167651 CGAACCTTTA AGAGCACGCT TTGCTTTTAG TCGGAGACTT TCCTATTACT  
167701 CGGATCAAGA TCTAAAAGAG ATTTTAGTCC GCTCCTCACA TTTACTCGGA  
167751 ATCGAAGCTG ACAGCTCCGC ATTACTAGAA ATTGCTAAGA GATCCCAGG  
167801 GACGCCACGA CTGGCAAATC ATCTTCTACG TTGGGTCAGA GATTTTGCTC  
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168251 GATACTTTTG TGAAGCAGGA TACTGTCGTT GAACCTAAAA TTCGTGTCCT  
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168501 TTTTAAACGG GATTCAGTAT CAAGGTTCCC TATACGTTCA TCGTAAAGAC  
168551 AACCATTGCA TCATGGTTTC TAACGAAGTT ACAATCGAAG ATTATCTGAA  
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WO 00/27994

PCT/US99/26923

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168801 GGACAGCTCG TTTAGTTGTG GATAGCCCTC AAGGATTAAT TATAGATGCA  
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168901 TGCACGTCAG ATTCTTGAGA AGTTCTACAA GGATGTGGAT TTTGTAGTTA  
168951 TAGAATCCTG GAATGAAGAA CTGGACGGAG AGATCAGGTA ACCTCTTTTCG  
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169051 GTTGCTACAT TTTGAGGGAC AAACCCTTGC TGA CTCTCGG CAACTATTTG  
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169901 TCGCAAGTAA AGGATCAAAA GAAATCGCCT CTAAAACAGG AGCGAATTGT  
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WO 00/27994

PCT/US99/26923

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170251 AAAGTTTTAA ACTCTCTACT TGGAGCGCAA GGATCAGAGG CATAAGCATA  
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171001 CGCCAGAAAT ACAAGGGAGT TTTTGATTTT AAGCCTCTGA AATCGTTTAC  
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171301 AACTCAGAG GAAATTGGCC TTATATGAGA AATTATTAGA AGGATCTATG  
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WO 00/27994

PCT/US99/26923

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171501 ACCGTGTGTG CTGATATTTG TGCTGGTAGA GAACCTTCTG TAGATACAAT  
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172451 CGGGGAGATT GAACTCCTTT ATAGTAGTCC TAAAGCTAAG GAAAAACGCA  
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172601 CACAGTCAAT ATCATCTTAC CTACAATTTT TGAATTGCGG CTTTCTGCCG  
172651 AAGAATTCTT AGTGGGGTTG TCCTCAGGAA TTTTGTCTT AAAGTATGAC  
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WO 00/27994

PCT/US99/26923

172751 AGTCACGGTT ATCGGTATCG TTCCCAAAT GCGGATGCT ATCTTTAGGA  
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174001 AAGTTGCGGC TAAACGTACG GTTAAAAAAG CTACTGTTCG CAAAACCGCT  
174051 GTAAAAAAC CTGCAGTTTC TAAGACGGCT GCTAAAAAGA CAGTAGCAAA

WO 00/27994

PCT/US99/26923

174101 GAAGACTACA GCTAAGAGAA CAGTTCGTAA GACTGTTGCT AAGAAGCCTG  
174151 CAGTTAAGAA AGTTGCTGCT AAACGTGTAG TAAAAAGAC AGTAGCAAAG  
174201 AAGACTACAG CTAAGAGAGC GGTTCGCAAG ACTGTTGCTA AGAAGCCTGT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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219901 AGATCCAGAG TCTCCTTGC CACAACCTCA AGAGAGGCTA CAGCTTGGGG  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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226901 AAAGGATCAG ATGTGCTTTA GGAAGAGCG TTGAAGGGT GAACATGGAT  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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233201 CTGTAGACCA TAGACGCTTG GTCAACATAT TAGGGAAAA TCTTCTTTTA  
233251 GTCTTCCCTG TCACTTTCAA ACCAATTCCT TTTTCTTTT TAGCAATACC  
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233351 ACTTTCTTGA CATATTCTTC CTATGAATTC TCTAACATCC GCTCAATAAA  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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245901 GACTGGAGCA GGTTCAGATG TATCCACTGG AATATGAGCA GAAGACTCTT  
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246051 GGCAAGAGCT ACTTTTACAG ACTTTTCTTT CGCAGAAGGT TTTTCTGAAG  
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246901 AACTTCCGCT CCACCATTTT CAGACTCTTG AACTTCATAG AGTAGGGCGT  
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WO 00/27994

PCT/US99/26923

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247101 ATTCTTCATA AATAACGTCT CTCTCAGCAT GTCTTAGCTT TTGACCGATA  
247151 ATTTGTCGTG CTGCGTGAGC AGCTATCTTC CAAAATTATC AGAAACAAAA  
247201 GGGACATCCA TGTACTGACC AATCTGACAG TCCGGATCGT ATTCTCTGGC  
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247301 CCTTTTCACA AAAGACTTCG ATGTCACCAG TACGAGAATT AATGTTTACA  
247351 GATATGTTTCG CGTCATCTCT TAAGGTTTTT TTAGCAGCAA TTTTAAAGC  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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251301 ATATGAATGA TTTCCATAGA GTTCGCACTA ATTCCTTCA GGATTTTCCA  
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WO 00/27994

PCT/US99/26923

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253301 TAGTTGTTGA GTTTCGTAAC AATAAAGAGC CTTTAGTATT TCTAGGTGAG  
253351 TACGCACAAG GAAGAATTTT CAATAAAGAT AGCACGATCT TTGGTACAGC  
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253651 AGCATTGTGA ATGAAATTGG TTTTGATAGG GATTTAGCTT CAGAGAAATC  
253701 TCCTGAAGCT CTTTTCCCTG GGCTGTCTTC AAAACTTCCT GATGGCCAAC

WO 00/27994

PCT/US99/26923

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253851 GGTTTCAGGA AGAGAGCTAG CGACTCCTGT GGCTTTAAGA TACCGAGTTC  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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259051 TGAAAGAAAA CCCTAATCAA GATGTCGTCC CTACAACAGT AATTTTTTCT  
259101 GGTAAGGCGG CTCCTGGCTA TGTCATGGCC AAACATTA TCAAGTTAAT

WO 00/27994

PCT/US99/26923

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259301 TTCTGGAACA GGAAATATGA AATTTGCTTT GAATGGAGCT CTGACTATAG  
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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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WO 00/27994

PCT/US99/26923

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271951 ATCTATTATA AATGTGGCTT CTATTGTTGC TAAGATCGGT AGTGCGGGCC  
272001 AGACCAACTA TGCTGCTGCT AAAGCTGGGA TTATTGCTTT CACAAAATCT  
272051 TTAGCTAAGG AAGTAGCTGC AAGAAATATT CGTGTCAACT GCCTTGCTCC  
272101 AGGCTTTATT GAAACAGACA TGACAAGCGT GTTGAATGAC AATTTAAAG  
272151 CTGAGTGGCT TAAGTCGATC CCTTTAGGTA GGGCTGGCAC TCCAGAAGAT  
272201 GTTGCTCGTG TGGCGTTGTT TTTAGCCTCG CAGTTATCGA GCTATATGAC  
272251 CGCGCAGACA CTGGTTGTTG ATGGGGGATT GACTTACTAA GACAATAGAA  
272301 GAAAGGGATT TGAAAATTC TCTTCGAGAA CTAATTAAGT AACCGTCGAA  
272351 TAAAAAATGA TTTTTTGCGA TACTAATTCT CTTTCTCTTT GTCCCTAGGG  
272401 AATAGTGAAG TATTGTATAG TTTAAATAGT AAAAGGATAT AAGCAATGAG  
272451 TTTAGAAGAT GATGTAATAG CAATTATTGT TGAGCAGTTA GGAGTGGATC  
272501 CAAAAGAAGT TAATGAGAAC TCTTCTTTTA TTGAAGACTT GAATGCTGAT  
272551 AGTTTAGATT TAACAGAATT GATTATGACT TTAGAAGAAA AATTGCTTT  
272601 TGAAATTTCA GAAGAAGATG CTGAGAAGCT TCGTACTGTC GGGGATGTAT

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272651 TTACTTATAT TAAGAAACGT CAAGCTGAAC AATAAACTTT CTTATATTCT  
272701 GGGTGCGTCG TAATCTTTTT TAAAGCTATT GTTTTCAAT AGTGATTACG  
272751 GCGTGCCTTT TTTTCTATAG AGTAGCTCAT CTAGAAAGAT TTATTTTGTC  
272801 TTTTAAAGGT TCTCTGAACT TGATTGTTT AGCATAGAGC TCTAAAAAG  
272851 ATAAAGCTAC GGATGGGCAC TCTTCCACAA TGTTTAGAAT TTGTCCTTTG  
272901 CTAAGAACTA GCATGCGGAC TTGTGTATTT GCAGAAGCAT TGTATTCCCT  
272951 GGGCTTATTA TTGAATAAGC TTTCTCTCC AAAACAATCT AAAGGTTTTA  
273001 AATTTAGAGG AGACTCTAGT TTTTCTTTAG AGATCGTAAT GTATCCTTCT  
273051 ACAATGATAT AAAAGCTGAA TCCAGGTTGT CCTATAGAGA ATACATTGCT  
273101 GCCAGGCTTA AATATTATCG TTTTCAAGTTT ATCGGCAATT GTTAAAAGAA  
273151 GGTCCATGTC TAAAGATTGG AATATAATCG TTTTTTTATAG TAGAAAGGCG  
273201 CGATCGATCA AATTCATAAA AAAGTTCCTT ATTCACACCA TAGTTTTAGT  
273251 TTTT

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